

## FIGURE 1

GGGGCTTCGGCCGACGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGT  
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCGAGTTTTATGCATTG  
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCTCGAAGAGAACGTTATCATCAAA  
TTAAACAAGGCTGGCCTTGTAAGTCTGGAATACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACCT  
CCAGAAAACAACCCTTTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT  
TATATATGTTTGTTCAGACCATCCTTTCCACCAATGCAGCCCCAAAATCCATGGCAAACAAGT  
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTC  
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG  
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCTTCTTT  
GGTTTTTCTTGACTTACATTTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA  
TGGATTAACCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA  
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG  
TTCACAGAAGTTGCTTATCTTCTCTGAAATTTCAACCACCTTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT  
ATG

**FIGURE 2**

<subunit 1 of 1, 266 aa, 1'stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIIVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG  
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAAEWSSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

**Important features:**

**Type II transmembrane domain:**

amino acids 13-33

**Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

**N-myristoylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

**FIGURE 3**

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC  
 GTGTGAGGGGGCCTGTGGCCCCAGCGTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC  
 CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG  
 GATTTGGGTGGCTTTTCTTCATGCGCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAG  
 GTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATCTTGAAATCTTAGG  
 AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATCTGCTGATCCTGG  
 TTTTCATGGTGCCCTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGA  
 CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCC  
 CATTCTCAGCCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG  
 TGACTCTCATGGCTCTTCTTCTGGATTTGGTGTGTCAACTGCCCATACTTACATGTCTTACTTC  
 CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT  
 CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA  
 AACCATCAGGTTTCTGGGGAATGATAAAAAGTGTACCCTTCAGCATCAGGAAGTGAATCTTACT  
 CTTATTCAACAGGAAGTGGATGCTTTTGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCT  
 ATATGCTACCAAGGAGAGAATAGAATACTCCAAACCTTCAAGGGGAAATATTTTAATTTCTTGGTT  
 ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTGATCGAGTT  
 GGGAAAACGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT  
 GAAGTTTTGGTCCCAACACATTTCTTCATTCTGTTGGAATAATCATCGTCACATCCATCAGAGGAT  
 TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCATTGTCTTG  
 CTATTAGCACAGATAATGGGCATGTACTTTGTCTCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT  
 AGAATACCGCACCATAATCACTGAAGTCCTTGGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTTTG  
 ATGTGATCTTCTGGTCAAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCA  
 GAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAAATTTA  
 GATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAACAACAAAATGCTATGGTAGC  
 ATTTTTACCTTCATAGCATACTCCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAG  
 AACATGAGAGGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG  
 TGTAGAGGCGGAGAGGAGCCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT  
 CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTTAAGGTTTACATGGAAAAGGTTATAGCTTTG  
 CCTTGAGATTGACTCATTTAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCG  
 ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

**FIGURE 4**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV  
LNSSSRYPFHWMNLCVILLILVFMVFPFYIGYFIVSNIRLLHKQRLLFSCLLWLTMYFFWKLGBP  
FPILSPKHGILSIEQLISRVGIVGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQ  
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDLEELSRQ  
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDVPVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLLAQIMGMY  
FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

**Important features:****Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160



**FIGURE 5**

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC  
 AGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT  
 GTTTCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT  
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTCCATCCAGGT  
 GTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG  
 AAGCTAAGGAGGCCGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC  
 TTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTTCATCTCTAG  
 GATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGATTGGAAGGTTCCAGTGA  
 GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCATTCCAGAA  
 ATTATCACCACCAAGATCCCATTCAACACTCAAACGCAACACAAACAAGAGATTTATTGT  
 CAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCCTC  
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTACAGAAAGTTTTATG  
 GAACTAGCACCATTGTCTACAGAACTGAACCATTTGTTGAAAAATAAGCAGCATTTCAAGAATGA  
 AGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGCTCTCCTCTTCTTTGGTGCTG  
 CAGCTGGTCTTGGATTTTGCTATGTCAAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAT  
 CAGCAGAAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCATA  
 TGAGGAATCAAAGAAAAGTATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGC  
 GATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTT  
 CATGCTCCTTACCCTGCCCGAGCTGGGGAATCAAAGGGCCAAAGAACCAAGAAGAAAGTCCA  
 CCCTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT  
 GCCCTTCTCCTTATTGTAACCCGTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCT  
 TTCTAGCCTGGCTATGTCTAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGAAGGAC  
 CTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGGTG  
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCTTTCTTCA  
 GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAAGAGCAAAAGAA  
 GGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAA  
 GCTAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAAC  
 ACAGACAGGGTCAAAGTGTCTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA  
 CTTACTTTTTCTGGTCTCTACCCTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA  
 AAAATAAAAACTCTTATAAATTTCTATTTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT  
 ACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAAACATTTGCTGAATAGCTACTATATGTC  
 AAGTGTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTCACATAGTAG  
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAACTAAT  
 TTTTATTTTTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAAT  
 TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAAGCACATTTTAAAGTGCC  
 ATTAACAAATGTATCACTAGCCCTCCTTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATT  
 TGTGACAAAAAATTAAAGCATTTAGAAAACCT

## **FIGURE 6**

MARCFSLVLLLSIWTRLLVQGSRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG  
 LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN  
 SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR  
 RKKLICVTEVFMETSTMSTETEPFVENKAAFKEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK  
 RYVKAFFFTNKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

**FIGURE 7**

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCGCTCCCGCATCTGCACCCGAGCCCGGC  
GGCTCCCGGCGGGAGCGAGCAGATCCAGTCCGCGCCGCGAGCGCAACTCGGTCCAGTCGGGGCGG  
CGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGG  
CGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCCGGCCCG  
GCTCTCAGCTACCCGAGGAGGAGGCCACCCTCAATGAGATGTCCGCGAGGTGAGGAACTGAT  
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGTGCTA  
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTATCACAATGAGACCAACACAGAC  
ACGAAGGTTGGAATAATACCATCATGTGCACCGAGAAATTCACAAGATAACCAACAACCAGAC  
TGGACAAATGGTCTTTTCAGAGACAGTTATCAGATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC  
ACGAGTGCATCATCGACGAGGACTGTGGGCCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC  
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGCTGTGGAGACCA  
GCTGTGTGTCTGGGGTCACTGCAACAAATGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACA  
ACCAGAGGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCCTGTGTTCCCTGTGTGC  
ACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC  
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCTCCTCTGCCAGC  
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG  
GAGATCCTGCTGCCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG  
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGGCTG  
CCGCCGTGCACTGCTGGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA  
TAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGGCTGACCAGGCTTCTTCCTA  
CATCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTACAGT  
CCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAACTGCA  
GGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCCTTACCAGTTGGCAGACAGCCG  
TTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGGAGTCTCCCTC  
TGATTGGTTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTTGCAAACATCAACCTGGCAAAAATG  
CAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC  
AGATGAAATGTTCTGTTCAACCTGCATTACATGTGTTTATTCATCCAGCAGTGTGCTCAGCTCC  
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGG  
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGTCTCT  
CTCCACTACCCACACAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAGAGATGGGAT  
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAATAATTCTCACATCCCTCTAAAAGTAAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGAT  
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAACCGAGCAGGGC  
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG  
TTTTCAGGTGTATGGACTGTTGCCACCATGTATTCATCCAGAGTCTTAAAGTTTAAAGTTGCA  
CATGATTGTATAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAA  
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 8**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL  
RSAVEEMEAEAAAKASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMFSE  
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMMLCTRDSECCGDQLCVWGHC  
TKMATRGSNGTICDNQRDCQPLCCAFQGLLFPVCTPLPVEGELCHDPASRLDLITWELEPDG  
ALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE  
RSLTEEMALGEPAAAAAALLGGEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

**FIGURE 9**

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC  
GGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCAGGGCTACTCATCCAAAG  
GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTCTGGACCTT  
AACTGGGTACTGGCCCTGGGCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC  
ACACTGGGTCAATTGGCATTGAGCCCTCATCTGACCCTTGTGCAGATAGCCGGGTCACTTG  
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGCCCGCTGCATCATGTGCTGTTT  
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCCAAAC  
ATTGTCAGGGTGGTCTGCTGGACAAAGTCACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT  
GGTCGGAGGCGTGGGGGTCCTGTCCTTCTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG  
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCCTAT  
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCCT  
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA  
AGATTCTGGGCAAGAAGAACGAGGCGCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG  
CCCTGATCCAGGACTGCACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT  
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACT  
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG  
AAACCTCCGTCTCTATTAATAAATAAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTATCCCA  
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAA  
AAGATTTTATTAAAGATATTTTGTAACTC

**FIGURE 10**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGFLFWTL  
 NWVLALGQCVLAGAFASFYWAFHKPDIPTFPLISAFIRTLRYHTGSLAFGALITLVQIARVIL  
 EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN  
 IVRVVVLDKVTDLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY  
 VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKNEAPPDNKKRKK

**Important features:****Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

**N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

**Hypothetical YBR002c family proteins.**

amino acids 276-288

**Ammonium transporters proteins.**

amino acids 204-231

**N-myristoylation sites.**

amino acids 60-66, 78-84

**Amidation site.**

amino acids 306-310



**FIGURE 12**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLI FTFFLFLGVLVSIIMLSPGVESQL  
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSWNQRWLKAE  
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVSIAAVLPKV  
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI  
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVAACEGRAFDNEQDGVITYSY  
SFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICASWAGLLLYLWTLVAPLLLRNRD  
FS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444



**FIGURE 13**

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCAACCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA  
 GGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG  
 CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA  
 CTCATGGCCAGGATTGAGTCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC  
 TTTCTGTTTGTGTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG  
 TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT  
 TTTGATATATTTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCATATGCTGTGTGCAG  
 ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAAG  
 TGATCCTTTTGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTTCATTCATC  
 CTTGCCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA  
 CAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG  
 GTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT  
 GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTAAATGTGAAAAACCTCACAGAAAGTC  
 ATCGAGGCCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTCGACAGTAAAGTTGAAATGGTGACGTC  
 CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAAACGTTGTAC  
 CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT  
 TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTCGTGATTCCCTAATC  
 AAAAGACTTAATATATTGAAGTAACACTTTTTTTAGTAAGCAAGATACCTTTTTTATTTCAATTCAC  
 AGAATGGAATTTTTTTGTTTCATGTCTCAGATTTATTTTGTATTCTTTTTTAACTCTACATT  
 TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTAAAAAGTGAATAAAATCTG  
 ACATGTCAATGTGGCTAGTTTTATTTTCTGTTTTGCATTATGTGTATGGCCTGAAGTGTTGGA  
 CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAATGTCACCAGACATTTGTATTATTT  
 TTATCATGAAATCATGTTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC  
 ACAAATGACTTAAACCATTATATCATGTTTCCTTTGCGTTTCAGCCAATTTCAATTAATGAA  
 CTAATTAATAA

## FIGURE 14

MNHLPEDMENALTGSQSSHASLRNIHSINPTQIMARIESYEGREKKGISDVRRTFCLFVTFDLLF  
 VTLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT  
 AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQAEENRLLIVQDASER  
 AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

### Important features of the protein:

#### Signal peptide:

amino acids 1-20

#### Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

#### N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

**FIGURE 15**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGACCCGCCAGGAAAGACTGAGG  
 CCGCGGCCTGCCCGCCCGGCTCCCTGCGCCGCCGCCGCTCCCGGGACAGAAGATGTGCTCCAG  
 GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGGGCTGCCCAT  
 CCGGCTGCCAGTGCCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACACGGTGCCC  
 CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC  
 AGGCAGCTTTGCCGGCTGCCGGGCTGCGAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCC  
 TGCCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG  
 CATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCTCGAGCGCCTCTACCTGGGCAAGAA  
 CCGCATCCGCCACATCCAGCCTGGTGCTTCGACACGCTCGACCGCCTCCTGGAGCTCAAGTGC  
 AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCCTGCCCCGCTGCTGCTGCTGGACCTCAGC  
 CACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCT  
 GGCTGGTCTGGGGCTGACGAGCTGGACGAGGGGCTCTTACGCCGCTTGCGCAACCTCCACGACC  
 TGGATGTGTCCGACACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCCTCCGGGGCTGACG  
 CGCCTGCGGCTGGCCGGCAACACCCGCATTGCCAGCTGCGGGCCGAGGACCTGGCCGGCCTGGC  
 TGCCCTGACAGGAGCTGGATGTGAGCAACCTAAGCCTGCGAGGCCCTGCTGGCGACCTCTCGGGCC  
 TCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGC  
 TGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACTAGGCCAGCCCTGAGGAGACGCGCTGCCA  
 CTTCCCGCCCAAGAAGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCCAG  
 CCACCACCACCACAGCCACAGTGCCACCACGAGGCCCGTGGTGCGGGAGCCACAGCCTTGTCT  
 TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTC  
 CACTGGCCCCACGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA  
 ATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTTCAGG  
 GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAG  
 GCCACCACGGTCCCTGACCCTGGGCATCGAGCCGCTGAGCCCCACCTCCCTGCGCGTGGGGCTGC  
 AGCGCTACCTCCAGGGGAGCTCCGTGCGAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG  
 GGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCAACCA  
 GCTGCGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGGCCGAGG  
 GCGAGGAGGCCTGCGGGGAGGCCCATACACCCCGAGCCGTCCACTCCAACCAGCCCCAGTCACC  
 CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC  
 GCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGCGGGGGCGGGCCATGGCAGCAGCGGCTCAGG  
 ACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAACCTGGAGGGAGTGAAGGTCCCTTGGAG  
 CCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGTCTGAGTGTGAGGTGCC  
 ACTCATGGGCTTCCAGGGCCTGGCCTCCAGTCAACCCCTCCACGCAAAGCCCTACATCTAAGCCA  
 GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC  
 ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCGAGACAGGGCTGTGTGACCACAGCT  
 GGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC  
 CTAACGTCCCCAGAACCGAGTGCCATATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC  
 CTTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGTCTGCTGGGCTCTCCAC  
 TCCAGGCGGACCTTGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGGAGAGCGGGTAGGC  
 GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGC  
 TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATCT  
 GGGAAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAA  
 GGCTTTTGTAAAGAAAAATAAAAGATGAAGTGTGAAA

**FIGURE 16**

MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDVPPDVTGLYVFEENGIT  
 MLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
 LGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEPGILD TANVE  
 ALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL  
 AGLAALQEELDVSNSLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRESHVTLASPEE  
 TRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAP  
 SPPSTAPPTVGPVPQPDQCPPSTCLNGGTCHLGRHHLACLCPEGFTGLYCESQMGQGRPSPTP  
 VTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY  
 TVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV  
 LLAALAAVGAAYCVRGRAMAAAAQDKGVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSE  
 CEVPLMGFPGLQSPHAKPYI

**Important features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 579-599

**EGF-like domain cysteine pattern signature.**

amino acids 430-442

**Leucine zipper pattern.**

amino acids 197-219, 269-291

**N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

**Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

**N-myristoylation sites.**
 amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
 594-600, 640-646

**FIGURE 17**

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG  
 GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCCTCGG  
 ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA  
 AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGA  
 ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTACAG  
 AAGATATCAGCTTTCTAGAGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA  
 CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT  
 TTTCTTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTG  
 CTACAACCTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCT  
 AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAG  
 CAATAAGAAAAGCCAAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
 CCAAAGCCCTGGAGAGAGTGTCTATGCTCTTTTATTGGTGATTACTTGCCACAGAATATCCAG  
 GCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCAAGGGACAGACTGCTCTTGG  
 CTTTCTGTATGCCTCTGGACTTGGTGTTAATTCAAGTCAGGCAAAGGCTCTTGTATATTATACAT  
 TTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTTTAGTGGAAGGCT  
 AATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTTTTCAGCTTTCATGATC  
 CAGATTTGCTTGTATTAAGACCAAATATTCAGTTGAACCTTCCTTCAAATCCTTGTTAATGGATAT  
 AACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACAATTTTCTTTAAAATGATTAG  
 TTTGGCTGATTGCCCCTAAAAAGAGAGATCTGATAAATGGCTCTTTTAAATTTCTCTGAGTTG  
 GAATTGTCAGAATCATTTTTTACATTAGATTATCATAATTTTAAAAATTTTCTTTAGTTTTTCA  
 AAATTTTGTAATGGTGGCTATAGAAAAACAACATGAAATATTATACAATATTTGCAACAATGC  
 CCTAAGAATTGTTAAAATTCATGGAGTTATTTGTGCAGAATGACTCCAGAGAGCTCTACTTTCTG  
 TTTTTTACTTTTCATGATTGGCTGTCTTCCATTTATTCTGGTCATTTATTGCTAGTGACACTGT  
 GCCTGCTTCCAGTAGTCTCATTTTCCCTATTTTGCTAATTTGTTACTTTTTCTTGCTAATTTGG  
 AAGATTAACCTCATTTTAAATAAAATTATGTCTAAGATTAAAAA  
 AA

**FIGURE 18**

MRVRIGLTLLLCVLLSLASASSDEEGSQDES LDSKTTLTSDSVKDHTTAGRVVAGQIFLDSESEL  
 ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEPPKKVRKPALTAIEGTAHGEPCHFPFLFLDK  
 EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEAARRQMQEAMMYQTGMKILNGSNKKSQKR  
 EAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMF EKLTEEGSPKGQTALGFLYASGLGVN  
 SSQAKALVYYTFGALGGNLIAHMLVLSRL

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

**Tyrosine kinase phosphorylation site.**

amino acids 220-228

**N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

**Glycosaminoglycan attachment site.**

amino acids 267-271

**Microbodies C-terminal targeting signal.**

amino acids 299-303

**Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

**Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

**FIGURE 19**

AATTCAGATTTTAAGCCCATTCCTGCAGTGGAATTCATGAAC TAGCAAGAGGACACCATCTTCTT  
 GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGAAAAATGCTCTTTTGGGTGCTAGG  
 CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAACTAAAGATTGAAGACATCACTG  
 ATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACTTTTGAT  
 AAAAAGGGATTCATGTAATCGCTGCCTGTCTGAÇTGAATCAGGATCAACAGCTTTAAAGGCAGA  
 AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG  
 CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGTT  
 CCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
 CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG  
 TTATTAATGTCTCCAGTGTTGGAGGTCGCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA  
 TATGCAGTGGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC  
 ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC  
 TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAACAACAATATGGAGAAGGTTACATTGAAAAA  
 AGTCTAGACAAACTGAAAGGCAATAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG  
 CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA  
 TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA  
 GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA  
 AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT  
 CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT  
 CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTTGCCCT  
 GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATGA  
 TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTTAAGT  
 ATCATCTCTTATCTAAATATTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGPHVIAACLTESG  
 STALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY  
 REPIEVNLFGLISVTNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDLSLRDMK  
 AFGVHVSCIEPGLFKNLADPVKVEKKLAIWEQLSPDIKQYGEYIEKSLDKLKGKNSYVNMD  
 LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLKQKAEIANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212



**FIGURE 21**

CTGAGGCGGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG  
 CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTCTTCTTGGGGAAGTAAAA  
 GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA  
 CATTGAGAAATATATTCCATGCTATCAGCTTTTGTAGCTTTTATAATTCTTCAGGCGAAGTAAATG  
 AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCGGT  
 CGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTGCAGGAGCATTT  
 TTCAAACCAAGACCTTGTTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC  
 ATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTTTTTTCACAGGGTACCTTTAGTGGTT  
 GCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAACTGTATCAGGTTCCGTGTATGTCCACTGG  
 TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG  
 TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAGAGTATATGCAAAAAAGTG  
 GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAACGAGAAATTGA  
 GAAAGGAGAGGAGCACAGATTGAGGAGCAAGAGAGAAGAATCCAAAAAGACCTCAGGAGA  
 ACATTTTTCTTTGTGAGGATTACGGACCTTTTTTCCAAATTCTGAATTTCTTCATTCATGTGTT  
 ATGTCTTTAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACAACCACCATCTCGATGTAGT  
 AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC  
 AAATCATTAAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA  
 GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAAAT  
 GAGCAGCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC  
 CTACATTTGATCCTTTTAACCTTACAAGGAGATTTTTTATTTGGCTGATGGGTAAAGCCAAAC  
 ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTCCAC  
 TGTTTGACAGTAATACACAGATAACTCTTAGTGCAATTACTTCACAAAGTACTTTTTCAAACATCA  
 GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACCTAAGTTGTTGAGGGGAAGGCTTACACAG  
 ACACATTCCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT  
 TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT  
 GAGACCATGTCTATTAAAAAATAAAATGGAAAAGCAAGAATAGCCTTATTTTCAAATATGGAAA  
 GAAATTTATATGAAAATTTATCTGAGTCATTAAAATCTCCTTAAGTGATACTTTTTTAGAAGTA  
 CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT  
 AAAATTTAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLEVKGEAKNSITDSQMDDVEVYITIDIQYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKERRHSDQIMTFRERLLHKNLQEHFSNQDL  
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV  
QTHSSKFFEEEDGSLKEVHKINEMYASIQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDVVDNLTL  
MVEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDLDQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation sites.**

amino acids 75-79, 322-326

**N-myristoylation site.**

amino acids 184-154

**Growth factor and cytokines receptors family.**

amino acids 134-150

**FIGURE 23**

GGCACAGCCGCGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGACGAGCGGACCAGCGCAGGGCAGCCCAA  
GCAGCGCGCAGCGAACGCCCGCGCCGCCACACCTCTGCGGTCCCCGCGCGCCTGCCACCTTCCCTCCTTCCCC  
GCGTCCCCGCTCGCCGGCCAGTCAGCTTGCCGGGTTGCTGCCCGCGAAACCCCGAGGTCACCAGCCGCGCCTCT  
GCTTCCCTGGGCGCGCGCGCCTCCACGCCCTCCTTCTCCCTGGCCCGCGCCTGGCACGGGGACCGTTGCCTGA  
CGCGAGGCCCAGCTCTACTTTTCGCCCGCGCTCTCTCCGCTGCTCGCTCTTCCACCAACTCCAACCTCTTCTCC  
TCCAGCTCCACTCGTAGTCCCCGACTCCGCCAGCCCTCGGCCCGCTGCCGTAGCGCGCTTCCCGTCCGGTCCCAA  
GGTGGGAACGCGTCCGCCCGCGCCCGCACCATGGCACGGTTCGGCTTGCCCGCGCTTCTCTGCACCTGGCAGTGCTC  
AGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCACGCTTTTACGTGTCAAAGGCTTC  
AACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATCTGTCCCAGGGTTTACCTGCTGCTCT  
CAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTG  
CAAGCTGTCTTTGCTTACGTTACAAGAAAGTTTATGAATTTCTCAAAGAACTACTTGAAATGCAGAGAAATCCCTG  
AATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTG  
AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATG  
TTCCGCTGGTGAACCTCCAGTACCCTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG  
CCCTTCGGAGATGTCCCTCGAAATTTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTCGCTCAAGGC  
TTAGCGGTTGCGGGAGATGTGCTGAGCAAGGTCCTCGTGGAAGTAAACCCACAGCCAGTGATCCCATGCCCTGTTGAAG  
ATGATCTACTGCTCCACTGCCGGGCTCTCGTACTGTGAAGCCATGTTACAACCTACTGCTCAAACATCATGAGAGGC  
TGTTTGGCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTA  
GAGGGTCCTTTCAACATTTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGAT  
AATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATTTCTCGT  
TCCATCTCTGAAAGTGCCCTTCAGTGCTCGCTTCAGACCACATCACCCGAGGAACGCCCAACCACAGCAGCTGGCACT  
AGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTCGGTCTCCCTTCGAGCAAC  
GTTTGCAACGATGAGAGGATGGCTGCAGGAAACGCCAATGAGGATGACTGTTGGAATGGGAAAGCAAAGCAGGTAC  
CTGTTTGCAGTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCAGAGGTCCAGGTTGACACCAGCAAACCAGAC  
ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG  
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG  
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCTGGGGCA  
CAGGCCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGGTTATGCAGAGAGAGTGGAGATTAATTTCTCAAACCTGAG  
AAAAAGTGTTCATAAAAAGTTAAAAGGCACCAAGTTATCACTTTTCTACCATCTAGTGACTTTGCTTTTAAATGAA  
TGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTCTCATTAGTTTTGGG  
AGGAAAAGGGACTGTGCATTGAGTTGGTTCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGATAGGTACAGAA  
CTATAGTTAGTTGTGCATTTGTGATTTTATCACTCTATTATTGTTTGTATGTTTTTCTCATTTCTGTTTGTGGGTT  
TTTTTTTCCAACGTGATCTCGCCTTGTTCCTTACAAGCAAACAGGGTCCCTTCTTGGCACGTAACATGTACGTATT  
TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTATTATCATGTTATCTATTAAAGAAAAAGCCCAAAAGC

**FIGURE 24**

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRRLYVSKGFNKNDAPLHEINGDHLKICPQGST  
 CCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH  
 LYMQNSELFKDLFVELKRYVVGVNLEEMLNDFWARLLERMFRLVNSQYHFTDEYLECVSKYTE  
 QLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGL  
 VTVKPCYNYCSNIMRGCLANQGDLDFEWNFNIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN  
 MQDNSVQVSQKVFQGCQPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK  
 EKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNPEVQVDT  
 KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG  
 KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

**Important features:****Signal peptide:**

amino acids 1-22

**ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

**N-glycosylation site.**

amino acids 514-518

**Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

**N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

**Glypicans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

**FIGURE 25**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT  
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC  
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCTGAG  
AGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCTGTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA  
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG  
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC  
TTCTTCTCCCACTCACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA  
TGTTTTTCAAGATCATTTTGTTTGTTGCTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCT  
GTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT  
AGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT  
AAATGTCAAAAA

## **FIGURE 26**

MKVLISLLLLLPIMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM  
TVSGLPKKQCPCDHFKGNVKKTRHQRRHRKPNKHSRACQQFLKQCQLRSFALPL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

**FIGURE 27**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG  
 AGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTACCCTGCC  
 CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAAGCTACTTCCCCTACCTGA  
 TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG  
 ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC  
 CAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA  
 AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGCTCCT  
 GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACCTCTGGTGCTGTG  
 CTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC  
 TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTC  
 GAGCCACCTGGAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA  
 GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG  
 GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTCCCAAGCTCCAAGGCACTCATTTGCTCC  
 TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTA  
GCAGAATGAGAGAAGACATTTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC  
 AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG  
 AAACACTAGGACCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTC  
 CCAATGTTGTCCCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACAC  
 CCATGCGTCTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC  
 CCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG  
 ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGAA  
 ACCACG

## **FIGURE 28**

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMVLTTPKSNRKMESKKRELFSSQIKGL  
 TGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
 RQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFEPW  
 KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLVPVPHIMGKAVKQSFPSKALICSFPSL  
 QLEQATHQPIYLPPLRGT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207



**FIGURE 29**

CAATGTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGCTCGGTGCCCAGAAAGTCTCTTCTG  
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA  
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAA  
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTTCATTAAGAAATT  
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC  
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

### **FIGURE 30**

MLLTL LLLLLLLK GSCLEWGLVGAQKVSSATDAPI RDWAF FPFSLC L LPHRPAMTCSQAQPRG  
EGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

**FIGURE 31**

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTT  
 CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT  
 ATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAAATCATGTCGG  
 GAAGAGATAACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCCTTGGCCATGATGTTTACC  
 TTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTATTTTGGGATTGTTGTT  
 TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA  
 CAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG  
 CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC  
 AAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA  
 TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAACTGCAGGAGCTGCCCAGGTT  
 ATGGAAGGCGGCCAAGTGAATATAAGCCCCCTTTCGGGCATTCCGTACATGTGGTCGTACCATTT  
 AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAG  
 TGGTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCTGCTCTC  
 TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAG  
 GATTCGAGAATCATGTGTCATGTACATGCAAACGCACTGAAAGAACAGCAGCATGGTGCAATGT  
 CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC  
 AACCAGAATGCATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC  
 ATTCAAAATCTTGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA  
 TTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC  
 AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC  
 CCATAGTTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTCTCTGTGTTTGTGTTGATC  
 TGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA  
 AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGA  
 GGGAACAGAACTCCAGGCCATTGTGAGATAGATATCCCATTTAGGTATCTGTACCTGGAAAACATT  
 TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT  
 TTAAAAGACCTAATAAACCTATTCTTCCTCAAAA

## **FIGURE 32**

MSGRDTILGLCILALALSLAMMFTFRFITTTLLVHIFISLVILGLLFVCGVLWWLYDYDTNLSIE  
 LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFA  
 ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQTIA  
 GAVVTCYFNRSKNPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQLKEQQHG  
 ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD  
 FIIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVVHSFSLVFETVLDALFLCFA  
 VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

#### **N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

#### **N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

**FIGURE 33**

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTTAGA  
 ATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCATTCTGTGTGGT  
 GAAAATTTTTTGAAGGAAATTTGCCCTTCTTCAAACAAGGGTGTCTATTCTGATATTTATGAGGAC  
 TGTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCTTGTGTTTGTGGTGACTGGAGTAC  
 ATTCAAACAAAGAAACGGCAAAGAAGATTAAAGGCCAAGTTCACTGTGCCTCAGATCAACTGC  
 GATGTCAAAGCCGAAAGATCATCGATCCTGAGTTCATTGTGAAATGTCCAGCAGGATGCCAAGA  
 CCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACTCCAGTGTGTGTGGCGCTGCCG  
 TACACAGTGGTGTGCTTGATAATTCAGGAGGAAAAATACTTGTTCGGAAGGTTGCTGGACAGTCT  
 GGTTACAAAGGGAGTTATTCACCGGTGTCCAATCGTTATCCCTACCAGATGGAGAGAATCCTT  
 TATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAACTACCCATCAGCTCTTACATACTCATCAT  
 CGAAAAGTCCAGCTGCCAAGCAGGTGAGACCACAAAAGCCTATCAGAGGCCACCTATTCCAGGG  
 ACAACTGCACAGCCGGTCACTCTGATGCAGCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCCAC  
 CACCTTGCCAAGGCCATCCCCTTCTGTGCTTCTACCACAGCATCCCCAGACCACAATCAGTGG  
 GCCACAGGAGCCAGGAGATGGATCTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCC  
 AGAGCTGATCCAGGTATCCAAAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTTGGAGC  
 GGATGTCAGCCTGGGACTTGTTCCAAAAGAAGAAATTGAGCACACAGTCTTGGAGCCAGTATCCC  
 TGGGAGATCCAACTGCAAAATTGACTTGTCGTTTTTAATTGATGGGAGCACCAGCATTTGGCAAA  
 CGGCGATTCCGAATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTCTTGACATTGGCCCTGC  
 CGGTCCACTGATGGGTGTTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACCTCAAGACAC  
 ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAAT  
 GTAGGTCGGGCCATCTCCTTTGTGACCAAGAATTCTTTTCCAAAGCCAATGGAAACAGAAGCGG  
 GGCTCCCAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT  
 GACTTGGCAGAGAGTCAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGTGAAAATGAG  
 AAGCAGTATGTGGTGGAGCCCCAATTTGCAACAAGGCCGTGTGCAGAACAAACGGCTTCTACTC  
 GCTCCACGTGCAGAGCTGGTTTGGCCTCCACAGACCTGCAGCCTCTGGTGAAGCGGGTCTGCG  
 ACACTGACCGCTGGCCTGCAGCAAGACCTGCTTGAACCTGGCTGACATTGGCTTCGTCACTGCAG  
 GGCTCCAGCAGTGTGGGGACGGGCAACTTCCGCACCGTCTCCAGTTTGTGACCAACCTCACCA  
 AGAGTTTGAGATTTCCGACACGGACACGCGCATCGGGGCCGTGCAGTACACCTACGAACAGCGGC  
 TGGAGTTTGGGTTTCGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGGC  
 TACTGGAGTGGTGGCACCAGCACGGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA  
 GTCCAAGCCCCAACAAAGAGGAAGTTAATGATCCTCATCACCAGCGGAGGTCTACGACGAGCTCC  
 GGATCCCAGCCATGGCTGCCCATCTGAAGGGAGTGATCACCTATGCGATAGGCGTTGCCCTGGGCT  
 GCGCAAGAGGAGCTAGAAGTCAATGCCACTCACCCGCCAGAGACCACTCCTTCTTTGTGGACGA  
 GTTTGACAACCTCCATCAGTATGTCCCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCAC  
 AGCCTCGGAACTGAATTTCAGAGCAGGCAGAGCACCAGCAAGTGCTGCTTTACTAACTGACGTGTT  
 GGACCACCCACCGCTTAATGGGGCACGCACGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAAC  
 AAATGTCTTGTATTATTCTTTGCCATCATGCTTTTTTCATATTCCAAAACCTGGAGTTACAAAGA  
 TGATCACAAACGTATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACAT  
 TTTGACAATTGTTTTCAAAATAAATGTTCCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAG  
 AGCTTTTGTGAGATTTTAAAGTTGTTATTTCTGATTTGAACTCTGTAACCTCAGCAAGTTTACAT  
 TTTTGTGATGACAATGTAGGAATTGCTGAATTAATGTTTAGAAGGATGAAAAATAAAAAAAA  
 AA  
 AAG

**FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
 CQDPKYHVYGTDVYASYSSVCGAHVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSLSLPRWR  
 ESFIVLESKPKKGVITYPSALTYSSSKSPAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA  
 TPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKP  
 VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI  
 GPAGPLMGVVQYGDNPATFNKTHHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
 RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENKQYVVEPNFANKAVCRTNG  
 FYSLHVQSWFGLHKTILQPLVKRVCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN  
 LTKEFEISDTRIGAVQYTYEQRLFEFGFDKYSSKPDILNAIKRVGYWGGTSTGAAINFALEQL  
 FKKS KPNKRKLMILITDGRSYDDVRIPAMAHLKGVITYAIGVAWAAQEELEVIATHPARHSFF  
 VDEFDNLHQYVPRIIQNICTEFNSQPRN

**Important features:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 181-200

**N-glycosylation sites.**

amino acids 390-394, 520-524

**N-myristoylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
 431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

**Amidation site.**

amino acids 304-308

**FIGURE 35**

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC  
 CAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTTAATTAAGCATGGAAT  
 ACAGAAAACAACAAAAACTTAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCC  
 GGTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGTCTCCGACTACTACCCCGAGTGTA  
 AAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGAATGGCCTCGGCTCTCTGGACTGTCCTTCCGAGTA  
 GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGCTCACTCCTGAGTTTCTTTGTGATGTGGTAC  
 CTCAGCCTTCCCCTACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTA  
 CAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAAGTGTCTCATCAAAATCCATTTCTGGTCATT  
 TGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT  
 TGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAGAGGCTGAAAGGAAGACAAAATGTTGGC  
 ATTGTCCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTGTAGACACATATAATA  
 ACCTGACCTTGAAGACATTATGGCATTACAGTGGGTAACTGAGTTTGGCCCAATGCCAAGTACGTAATG  
 AAGACAGACACTGATGTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA  
 GAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATATTT  
 CTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTATATAATGTCCAGAGAT  
 TTGGTGCCCAAGGATCTATGAAATGATGGGTACGTAACCCATCAAGTTTGAAGATGTTTATGTCCGGAT  
 CTGTTTGAATTTATTAAAAGTGAACATTTCATATCCAGAAGACACAAATCTTTCTTTCTATATAGAATCC  
 ATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTT  
 TGGCAGGTGATGCTAAGGAACACCACATGCCATTATTAAGTTTACATTCTACAAAAAGCCTAGAAGGACAG  
 GATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTCAGTGTGCTGGCTT  
 ACACCTGAAGTGAAGTCAATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGG  
 CCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG  
 ACCAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAAGGGTGTACTGAGTTATAAGCTCA  
 CTAGGCTGTAAAAACAAAACAAATGTAGAGTTTATTTATTGAACAATGTAGTCACTTGAAGGTTTGTGTA  
 TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAAACTTCTTCACTGAAGTTATA  
 CTGAACAAAATTTTACCTGTTTTTGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATT  
 ATTATTTAAAATTACTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAG  
 TGAATCATTCCTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCACTCCA  
 TTAATGTAAAGTCATAGGTCAATTATTGCATATCAGTAATCTCTGGACTTTGTTAAATATTTTACTGTGGT  
 AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

**FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHF  
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EKEDKMLA  
LSLEDEHLLYGDIIRQDFLDYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFINTGNLVKYL  
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV  
KPIKFEDVYVGICLNLKVN IHIPE DTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

**Important features:**

**Type II transmembrane domain:**

amino acids 20-39

**N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

**Glycosaminoglycan attachment site.**

amino acids 239-243

**Ly-6 / u-PAR domain proteins.**

amino acids 23-37

**N-myristoylation site.**

amino acids 271-277



**FIGURE 37**

CGCTCGGGCACCAGCCGCGCAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTCTTCAGCTCCTTCTCATC  
 TCGTCCCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATGTGTCTGGGAGTGCTGTG  
 AATATGATCAGATTGAGTGCCTCTGCCCGGAAAGAGGGAAGTCGTGGGTTATACCATCCCTTGCTGCAGGAATGAGGAGAA  
 TGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAACTGCAAGAGCTGCCGAAATGGCTCATGGGGGGGT  
 ACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTG  
 GCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTTGTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTTCATGC  
 TAAACCTGGGTTTGTATCCAACTAAGATTTGTTCATGTTGAGTCTGGAGTTGACTACATGTGCCAGTATGACTATGTTGAG  
 GTTCGTGATGGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG  
 GATCCCTCACTCCACGTCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTATGAGGAGATCACAGC  
 ATGCTCCTCATCCCTTGTTCATGACGGCACGTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGC  
 TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCTTGGGGGCCAGTCAATGGGTACCAAGAAA  
 TAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATTTGGCACCCTGGTGTCTTTCTTTTGTAACTCCTATGT  
 TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAGGGAAACAGCCCATCTGCATAAAGCTTCCGA  
 GAACCAAGATTTCAGACCTGGTGAGAAGGAGATTCTTCCGATGCAGGTTCACTCAAGGGAGACACCATACACAGCTAT  
 ACTCAGCGGCTTCAGCAAGCAGAACTGCAGAGTGCCCTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGG  
 ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGT  
 CTGAGGACTGGGAAGTGGAGTGGGCGGGCACCATCTGCATCCCTATCTGCGGGAAAATGAGAACATCACTGCTCCAAAGA  
 CCCAAGGGTTGCGCTGGCGTGGCAGGCGCCATCTACAGGAGGACCAGCGGGTGCATGACGGCAGCCTACACAAGGGAGC  
 GTGGTTCTTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACGTGGTGGTGGCTGCCACTGTGTTACTGACCTGGGGAG  
 GTCACCATGATCAAGACAGCAGACCTGAAGTTGTTTGGGGAAATCTACCGGGATGATGACCGGGATGAGAAGACCATCC  
 AGAGCCTACAGATTTCTGCTATCATTCTGCATCCCACTATGACCCCATCTGCTGATGCTGACATCGCCATCCTGAAGCT  
 CCTAGACAAGGCCGCTATCAGCACCCGAGTCCAGCCATCTGCTGCTGCCAGTGGGATCTCAGCACTTCCCTCCAGGAG  
 TCCCACATCACTGTGGCTGGCTGGAATGTCTTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGG  
 TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACATGTT  
 CTGTGCCAGCTGGGAACCCACTGCCCTTCTGATATCTGCATCTGCAGAGACAGGAGCATCGCGGCTGTGTCTTCCGGGA  
 CGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA  
 CTGCTTTCACCAAGGTGCTGCTTTTAAAGACTGGATTGAAAGAAATATGAAATGAAGACCATGCTCATGCACTCCTTGAGAAG  
 TGTTTCTGTATATCCGCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTGGCCTGTGAACCTGGCT  
 GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGGTCCA  
 CTACTAGGACAGCCAATGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAGAAGACCATATACAAAACCTCTCCA  
 CTCCACTGACCTGGTGGCTTCCCCAACTTTCAGTTATACGAATGCCATCAGCTTGACAGGGAAGATCTGGGCTTCATGAG  
 GCGGCTTTTGAGGCTCTCAAGTTCTAGAGAGCTGCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCTT  
 TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCCCTTCCCATCTCTGTACACATTTTAAATAAAATAAGGGTTGGCTTCT  
 GAACATACAAA  
 AA

**FIGURE 38**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT  
 IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGDCMRGQ  
 VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII  
 KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC  
 ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE  
 KRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPVQVSRETPLHQLYSAAFSKQKLQSAPTK  
 KPALPFGDLPMPGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP  
 KTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL  
 KVVLGKFYRDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR  
 DLSTSFQESHITVAGWNVLADVRSPGFKNDFLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA  
 SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLFPKDWI  
 ERNMK

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**EGF-like domain cysteine pattern signature.**

amino acids 260-272

**N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

**N-myristoylation sites.**amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672**Amidation site.**

amino acids 56-60

**Serine proteases, trypsin family.**

amino acids 489-506

**CUB domain proteins profile.**

amino acids 150-167

**FIGURE 39**

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACGTGGCTTAATC  
 TGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTTGTCTAAAGGAGCTTGGCTGG  
 TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGCTTCTGTTGC  
 TGGTCTTGCCCTTGGCTCAGTCTGTAACTACATTGACAATGTGGGCAACCTGCACTTCTGTATTTCAGAACTCTGTA  
 AAGGTGCCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAAGATGGCTGTCCAGACGGCTGTGCGAGCC  
 TCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGAGCCTGGCCTAGACA  
 ACCCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACTTGGCCGGAGCAACCGAACTA  
 GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTCTTCGAA  
 GGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGGAAAAATCTGAAAAACCACTGCCCTGAAG  
 TCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAAATTACCAGCATCAAGATCAATCGAGTAGATCCCAGTGAAA  
 GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTTATCCAACACATTTATCGTGATGGGG  
 TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC  
 ACAACTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCCGCA  
 GCAGGAACAATGGACAGGCCCCGGATGCCTACAGACCCCGAGATGACAGCTTTTCATGTGATTCTCAACAAAAGTAGCC  
 CCAGGAGCAGCTTGGAAATAAACTGGTGCAGAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCG  
 GTGTGGCATATCGACATGGTCAGCTTGAAGAGAAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA  
 GCCCAGAAAGTGCGGCTCATCTGATTGAGGCCAGTGAAAGACGTGTTACCTCGTGTGTCGCCAGGTTTCGGCAGC  
 GGAGCCCTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCAGGGCCAGGGGAGAGGAGCAACA  
 CTCCCAAGCCCCCTCCATCTACAACTTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCTCG  
 GCATGACCGTCGCAGGGGGAGCATCACATAGAGAATGGGATTGGCTATCTATGTGTCAGTGTGAGCCCGGAGGAG  
 TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACTGACAGAGGTGAGCC  
 GGAGTGAGGCAGTGGCATTATTGAAAAAGACATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC  
 CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCT  
 GGGTCATGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC  
 TGGGCTTCTGCATTGTAGGAGGTTATGAAGAATAAATGGAACAACCTTTTTTCATCAAATCCATTGTTGAAGGAA  
 CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTGCTGTCAATGGTAGAAGTACATCAGGAATGA  
 TACATGCTTGCTTGGAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT  
 TTTTATAGAAATCAATGATGGGTGAGGAGAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACTATATTATC  
 TTGTCAGTTTTTATATTTAAAGAAAGAATACATTGTAAAAATGTCAGGAAAAGTATGATCATTAATGAAAGCCAGTT  
 ACACCTCAGAAAAATGATTCCAAAAAATTAATACTACTAGTTTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTAC  
 AACATTGTTTTATATTTTTCTATTCAATAAAAGCCCTAAAACAATAAAATGATTGATTTGTATACCCCACTGAATT  
 CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGTACATTATGGCCATTTTAAATTACAGCT  
 AAAATATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAACAAGAATAAATATTTTTTCAGAAGTTAAA

**FIGURE 40**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS  
 PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINR  
 ALSVLRRTKSGSAVANHADQGRESENTTAPFVFPRLYHLIPDGEITSIKINRVDPSSELSIRLV  
 GGSETPLVHII IQHIYRDGVIARDGRLLPGDIILKVNGMDISNVP HNYAVRLLRQPCQVLWLTVM  
 REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFIFNVLDGGVAYRHG  
 QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRSPDIFQEAGWNSNGSWSPG  
 PGRSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR  
 IKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP  
 SDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG  
 RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

**Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

**N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
 467-473, 603-609

**FIGURE 41**

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT  
 CTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT  
 TTCCACCTTTCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGTTGGGTGGGC  
 CACCAGTAATACTTCGTGGGTGCCATTCAAGAGATTCTTAAAGCAAAGGAGTTCATGGCTAATTTCC  
 ATAAGACCCTCATTTTGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT  
 GACAACTGTCCTTCTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC  
 TTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG  
 CTTTACAGAGGGTCGCCATCCTCGTTCCTCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA  
 CATCTGCATCCCTTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG  
 TAAAAAGTTTAAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTTGGG  
 ACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG  
 CATCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGG  
 GGGTGTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAATACTACTGGGGAT  
 GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGCCCCCTG  
 CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG  
 GATGAAGCTCTTACACCAAGTGTCACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT  
 TAGTATCTGTGGAACACAATCCCTTTATATATCAACATCACAGTGGATTCTGTTTGGTGCATGACCCC  
 TGGATCTTTTGGTGATGTTTGAAGAAGTGAATCTTTGTTTGCATAATTTTGGCCTAGAGACTTCAA  
 ATAGTAGCACACATTAGAACCCTGTTACAGCTCATTGTTGAGCTGAATTTTCTCTTTTGTATTTTCT  
 TAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAAACAAGACAGCTTTCTTAGTCATTTTGAT  
 CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA  
 AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATATGGGAT  
 AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA  
 AGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGTCAGGT  
 GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGA  
 GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC  
 CTTCAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT  
 TTTTAAAGAGTTTTTGTAAATGATTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT  
 ATTAATAATAATAATATGTCTATCAAATACCTCTGTAGTAAATGTGAAAAAGCAAAA

**FIGURE 42**

MGFNLT FHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYPQECKALQRVAILVPH  
RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV  
DLVPENDFNLYKCEEHPKHLVGRNSTGYRLRYSGYFGGVTALSREQFFKVNGFSNNYWGWWGED  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:****Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

**FIGURE 43**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG  
CCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCAACAG  
ACGGGACAACCTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT  
GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC  
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGAGAACCTACCTGCCCTGCCCCCGTCCCCCTCCC  
TTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGGCTGGTTCTTTGTTT  
TCCAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 44**

MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI  
CIFCCGCCHRSKCGMCKT

**Important features:****Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12



**FIGURE 45**

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC  
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT  
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG  
GACCTTCAACACAACCCCTCTTGTCACCATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAG  
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA  
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT  
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC  
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTCAGCAGAAACT  
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG  
GTCCTCCTGTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTGTACTGGGGCTATTTCTTTG  
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGACATTTGTGGG  
AAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT  
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA  
TCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCA

**FIGURE 46**

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP  
EGGTIIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK  
PKVTMGLQSNKNGTCVTNLTCCMEHGEEVDIYTWKALGQAANESHNGSILPISWRWGESDMTFIC  
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLLVPLLISLFLGLFLWFLKRERQEEYIE  
EKKRVDICRETPNICPHSGENTHEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLTMPDT  
PRLFAYENVI

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 224-250

**Leucine zipper pattern.**

amino acids 229-251

**N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295



## **FIGURE 48**

MTCCEGWTSCNGFSLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
 TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNANCEFSL  
 KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL  
 LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

### **Important features:**

#### **Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

#### **N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

#### **N-myristoylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

#### **TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12

**FIGURE 49**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGA  
CATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGAAGCCAATGACC  
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG  
CAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA  
CTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC  
TCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCCCT  
TTCTGATCAGGAGGCTTCTTTATGAATTAACTCGCCCCACCACCCCTCA

**FIGURE 50**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS  
SQKQHSFPVEKAIPILITPGSATTC

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 36-59

**N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

**FIGURE 51**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
 AGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG  
 AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG  
 GGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG  
 CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGAGACGCCCTGA  
 GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGAGGGGAGCTGGCTCTAAAGTCAGTGAG  
 GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC  
 AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA  
 TTGGCAGACAGGCAGAAGATGTCATTCGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG  
 GTGCTTGGCCACAGTGGTGCTTGGGAAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG  
 CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCG  
 GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA  
 GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCACTGAG  
 AGCCAGCAACCAGAATGAAGGGTGACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA  
 ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC  
 AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG  
 TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT  
 CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGA  
 CATAAACCCGGGTGTGAAAAGCCAGGGAATGAAGCCCGGGAGCGGGGAATCTGGGATTACAGGG  
 CTTTCAAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTG  
 GAGGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT  
 GGTGGAGTCAATACTGTGAACTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAA  
 GAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC  
 GCATCCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCACACTCCCTCCTTAA  
 AACACCACCCTCTCATCTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAA  
 AA  
 AA

## FIGURE 52

MKFOGPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVS  
 EALGQGTREAVGTGVRQVPFGGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGV  
 GHSGAWETSGGHGIFGSQGGGLGGQGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGGPPNF  
 GTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSSGGS  
 SSGSSSGSSSGSSSGSSSGSSSGSGSRGDSGSESSWGSSTGSSSGNHGSGGGNGHKPGCEKPGNE  
 ARGSGESGIQGRGQGVSSNMREISKEGNRLLGGSGDNYRGQGSWGSGGDAVGGVNTVNSETPGM  
 FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

### Signal peptide:

amino acids 1-21

### N-glycosylation site.

amino acids 265-269

### Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

### Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

### N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,  
 90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,  
 159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,  
 236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,  
 253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,  
 283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,  
 298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,  
 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
 387-393, 389-395, 395-401

### Cell attachment sequence.

amino acids 301-304



**FIGURE 53**

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG  
 CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT  
 ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTCCGCGCGGCTCCAGTGTTC  
 CACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACCTGGGCTGATCACTCCTACAGAGGAGGGC  
 TTGAAGGACTCGACCCAGATGTCGGCCACCTATCCCAGGGCTTTACGGTATGGCTGGGTCCCAT  
 CATCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGCTGCCA  
 TTGCACCCAAGGATAATCTCTTCATCAGGTTCCCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG  
 AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCTTCCATTTCACATCCT  
 GAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG  
 CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTA  
 CAGAAATGCATCTTCAGCTTTGACAGCCATTGTCAGGAGAGGCCAGTGAATATATTGCCACCAT  
 CTTGGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT  
 ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC  
 GCTGTCTATCCGGGAGCGGCGTCGCACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA  
 AGCCAAGTCCAAGACTTTGGATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG  
 CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACG  
 GCCAGTGGCCTCTCCTGGGTCCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG  
 ACAGGAGGTGCAAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCC  
 AGCTGCCCTTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATC  
 TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG  
 CCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGACC  
 CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCCTTTCTCCGCA  
 GGGCCAGGAACTGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCCTGGCGTTGAT  
 GCTGCTGCACTTCCGGTTCTGCCAGACCACACTGAGCCCCGCAGGAAGCTGGAATTGATCATGC  
 GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCATGACTTTTCTGAC  
 CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAAA

**FIGURE 54**

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFQPCKRNWFWGHLG  
 LITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP  
 WLGEIGILLSGGDKWSRHRRLTPAFHENILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
 SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC  
 RLVHDFDTAVIRERRRTLPTQGIDDFKDKAKSKTLDLFDVLLLSKDEDGKALSDEDIRAEADTF  
 MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
 LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP  
 LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
 VGLQ

**Important features:****Transmembrane domains:**

amino acids 13-32 (type II), 77-102

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

**N-glycosylation sites.**

amino acids 112-116, 168-172

**FIGURE 55**

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA  
GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT  
TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTGACGTGG  
TACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTTTTGCCGTGTGTCTTGC  
ATAATTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT  
GTAACATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGCAGCAATGTGTTGCTT  
GTGATTCGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAATCTTCCTCATGTACCTGTTTCCTC  
TCTGGATGTTGTCCCACTGAATTCCCATGAATACAAACCTATTTCAGCAACAGCAAAAAAAAAAAAA  
AA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFAR  
DAVKKCFVCLA

**Important features:**

**Signal peptide:**

amino acids 1-33

**Type II fibronectin collagen-binding domain protein.**

amino acids 30-72

**FIGURE 57**

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCAGCCAGCAGGCGGCCAACATGCTCTGTCTGTGCTG  
TACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCC  
ATTTTCAAGCTCAGTGTCTTCATCCCTCCAGGAATTCTCCACCTACCGCCAGTGGGAAGCAGAAAATTGTACAAGCT  
GGAGATAAGGACCTTGATGGGCGAGTACCTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGAGG  
CTGGTGTAAAGATTTTGGACAAAAGAATGATGGACGCATTGACGCGCAGGAGATCATGCAGTCCCTGCGGGACTTG  
GGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTCTCAAGAGCATGGATAAAAAACGGCAGCATGACCATCGACTGG  
AACGAGTGGAGAGACTACCACCTCCTCCACCCCGTGGAAAACATCCCCGAGATCATCTCTACTGGAAGCATTCACG  
ATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGCAGAGCGGGATGTGGTGAGA  
CACCTGGTGGCAGGAGGTGGGGCAGGGGCGGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGCTCATG  
CAGGTCCATGCCTCCCGCAGCAACACATGGGCATCGTTGGTGGCTTCACCTCAGATGATTCGAGAAGGAGGGGCCAGG  
TCACTCTGGCGGGGCAATGGCATCAACGTCCTCAAAATTGCCCCGAATCAGCCATCAAATTCATGGCTATGAGCAG  
ATCAAGCGCTTGTGGTAGTGACAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCTTGGCAGGGGCC  
ATCGCCAGAGCAGCATCTACCCAATGGAGTCTGAAGACCGGATGGCGCTGCGGAAGACAGGCCAGTACTCAGGA  
ATGCTGGAGTGCGCCAGGAGGATCTGGCCAGAGAGGGGTGGCCGCTTCTACAAAGGCTATGTCCCAACATGCTG  
GGCATCATCCCTATGCCGGCATCGACCTTGAGTCTACGAGACGCTCAAGAATGCCTGGCTGCAGCATTATGCAGTG  
AACAGCCGGGACCCCGCGCTGTTTGTGCTCTGCGCTGTGGCACCATTGTCAGTACCTGTGGCCAGCTGGCCAGCTAC  
CCCTTGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTCTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCTC  
TTCAACATATCTCTGGGACCGAGGGGGCTTCGGGCTGTACAGGGGGCTGGCCCCCACTTCATGAAGGTATCCCA  
GCTGTGAGCATCAGTACGTGGTCTACGAGAACCTGAAGATCACCTGGGCGTGCAGTGCAGGCTGAGCGGGGAGGGC  
CGCCCGGCGAGTGGACTCGCTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTTCTGTGAATGTGCCAACCT  
AAGCTGTCTCGAGCCAAGCTGTGAAACCTTAGACGCACCCCGAGGGAGGGTGGGGAGAGCTGGCAGGCCAGGGCTT  
GTCTGTGACCCAGCAGACCTCTGTTGGTTCCAGCGAAGACACAGGCATTCTTAGGGTCCAGGGTCAGCAGG  
CTCCGGGCTCACATGTGTAAGGACAGGACATTTTCTGAGTGCCTGCCAATAGTGAGCTTGGAGCCTGGAGGGCGGGT  
TAGTTCTTCCATTTACCCCTTGACGCCAGCTGTTGGCCACGGCCCTGCCCTCTGGTCTGCCGTGCATCTCCCTGTGC  
CCTCTTGCTGCCTGCCTGTCTGCTGAGGTAAGGTGGGAGGAGGGCTACAGCCACATCCCACCCCTCGTCCAATCCC  
ATAATCCATGATGAAAGGTGAGGTGAGTGGCTGCCAGGCTGACTTCCCAACCTACAGCATTGACGCCAATTTGGC  
TGTGAAGGAAGAGGAAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATG  
CTTGGGAGTGCAGGGGGCTCGGGCTGCCTGGCTGGCTGTCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT  
GGCCTGGACCTGTGAGGATGGGCCCCACCTCAGAACCAAACTCACTGTCCCCACTGTGGCATGAGGGCAGTGGAGCA  
CCATGTTTGAAGGGCAAGGGCAGAGCGTTTGTGTGTTCTGGGGAGGGAAGGAAAGGTGTTGGAGGCCTTAATTATGG  
ACTGTTGGGAAAAGGTTTGTGTCAGAAGGACAAGCCGGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG  
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGTTCCTGTCCAACCCAGCAGGGGCGCAGC  
GGGACAGCCCCACATTCACCTTGTGTCACTGCTTGGAACTATTATTATTTGTATTATTTGAACAGAGTTATGTCTCT  
AACTATTTTATAGATTTGTTAATTAATAGCTTGTCAATTTCAAGTTCATTTTATTATTCATATTATGTTTCATGGTT  
GATTGTACCTTCCCAAGCCCGCCAGTGGGATGGAGGAGGAGGAGAAGGGGGCTTGGGCCGCTGCAGTCAATCT  
GTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAGGCAGCAGCCCTGGCTCCTTTCTTTGGCAG  
GTTGGGGAAGGGCTTGGCCCCAGCCTTAGGATTTAGGGTTGACTGGGGGCTGGAGAGAGAGGGAGGAACCTCAAT  
AACCTTGAAGGTGGAATCCAGTTATTCTCGCTGCGTGCAGGGTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAG  
TGAGGTGCCTCTCACTGTGAATTTGTGGTGGGCGGGGCTGGAGGAGAGGGTGGGGGCTGGCTCCGCTCCCTCCAGC  
CTTCTGCTGCCCTTGTCTAACAATGCCGGCCAACTGGCGACCTCACGGTTGCACTTCCATTCCACCAGAATGACCTGA  
TGAGGAAATCTTCAATAGGATGCAAAAGATCAATGCAAAAATTGTTATATATGAACATATAACTGGAGTCTGCAAAAAA  
CAAAATTAAGAAAGAAATGGACGTTAGAAGTTGTCAATTTAAAGCAGCCTTCTAATAAAGTTGTTTCAAGCTGAAAAA  
AA

## FIGURE 58

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSI FKL SVFIPSQEFSTYRQWKQKIVQAGDKDL DG  
 QLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNG  
 TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGG  
 AGAVSRTCTAPLDRKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESA IK  
 FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAI AQSSIYPMEVLKTRMALRKTGQYSGMLDCARR  
 ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSTC  
 GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV  
 VYENLKITLGVQSR

**Important features:**

**Signal peptide:**

amino acids 1-16

**Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation sites.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

**FIGURE 59**

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC  
 TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
 CACTCATCATTGGCTTTGGTATTTAGGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCT  
 GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAACCTTTCTGATAT  
 CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG  
 AGCTGTCGGAGCAGGATGAAATGTTAGAGGCCGACAGCAGTGTGCTGATCAAGTGATAGTT  
 GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT  
 CATCACTTCTAAAGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG  
 AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC  
 CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATAC  
 CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA  
 TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG  
 ACAGAAATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT  
 CTCTTCTTTCTTTGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATGCTAAATTAAT  
 GTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC  
 CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
 AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAAT  
 CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTATGTGAAGTGAAGTGTGTTAAGA  
 GTGATAAGTAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
 CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGC  
 TGTAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCAC  
 AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG  
 GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC  
 TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT  
 CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 6a**

MASLGQILFWSIIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS  
 DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKC  
 YIITSKKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGAFSEVS  
 NTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLLNSKASL  
 CVSSFFAISWALLPLSPYMLK

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 258-281

**N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
 220-224

**N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194



**FIGURE 61**

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG  
 CACCAGGAGCCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGAGGGCAGTATGGTAGT  
 GGGCTACCCCCTGGTGGTGGTTATGGGGGTCTGCCCTGGAGGGCCTTATGGACCACCAGCTGG  
 TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAATCCAGGAGGACCATATG  
 GCGGTGCAGCTCCCGGGGGCCCCATGGTCAGCCACCTCCAAGTTCTACGGTGCCAGCAGCCT  
 GGGCTTTATGGACAGGGTGGCGCCCCCTCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC  
 GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
 ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA  
 GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGAAGAACCTCTT  
 CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC  
 AAATGGGCTACAACCTGAGCCCCAGTTCACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT  
 GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
 GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA  
 CCATGACAGCTTCTCGGATGCTATTGACCCAACCATCTGTGGAGAGTGGAGTGACACAGGGACCTT  
 TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC  
 ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA  
 AATAGTGAGGACCGGGCTGAGGCCACACAGATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGA  
 ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCCTTGTAATGG  
 AGTTAGTGTCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTGTTTCATCGGCCTGTTACC  
 GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCAAAGTGGAAAT  
 CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCTGCCACACCCATAAAT  
 CCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT  
 CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCT  
 TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAATTTGCATTTTTTTTC  
 ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

**FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSGTPGGPYGGAAPGGPYQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDS DH  
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK  
DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-  
66, 70-75, 78-83, 83-88, 87-92, 110-115

**FIGURE 63**

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC  
TCCCAGGCCTCTTTGCCCGGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACC  
AACTTGCTCAGCTCGGACAACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCGC  
TCTGGACCCTAGGTCTAATGACTTGGCAAGGGTTCTCTGAAGCTCAGCGTGCCTCCATCAGATG  
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCTGCCATG  
GATTCCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCTGGGGGA  
AGCGCTGCCTGAAGAACTCTCTTACCTCTCCAGTGCTGCGGCCCTCGCTCCGGGCAGTGGCCCTT  
TGCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC  
TCGGAGTCCAGACGACTGCCCCGTTCTAATTCACTGGGAGCCGGGGGAAAAATCCTTTCCCAACG  
CCCTCCCTGGTCTCTCATCCACAGGGTTCTGCCTGATCACCCCTGGGGTACCCTGAATCCCAGTG  
TGCTCTGGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGA  
ATCTGGGGTATCAATAATCAACCCCAGGTACCAGCTGGGGAATATTAATCGGTATCCAGGAGG  
CAGCTGGGGAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG  
GCAGCTGGGGGAATATTCATCTATACCCAGGTATCAATAACCCATTTCTCTCTGGAGTTCTCCGC  
CCTCTGGCTCTTCTTGGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG  
GGGCTAGAGCACGATAGAGGGAAACCCAACATTGGGAGTTAGAGTCCTGCTCCCGCCCCCTTGCTG  
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC  
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

**FIGURE 64**

MQGRVAGSCAPLGLLLVLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL  
 DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAAEDRLGEA  
 LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLLPRSNSLGAGGKILSQRP  
 PWSLIHRVLPDHPWGTNLNPSVSWGGGGPGTGWGTRPMPHPEGIWGINNQPPGTSGWNINRYPGGS  
 WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPPGVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
 259-264, 269-274, 270-275, 280-285, 281-286, 305-310

## FIGURE 65

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC  
TGGGCTGCCCCCTTGTCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA  
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGC  
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCTTCTTGGCCC  
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCCACCTC  
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

## **FIGURE 66**

MGSGLPVLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSGTSVTL  
HHARSQHHVVCNT

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 37-41

**N-myristoylation sites.**

amino acids 15-21, 19-25, 60-66

**FIGURE 67**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGG  
CAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGAGATGCGGTAGGAGGGGCGAGCGGAGAAGCCCC  
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCGGGCTGGGGCTGCTTCTGGCG  
CTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC  
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG  
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCACTAGCGA  
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT  
GCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA  
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA  
AGACTCTGCCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTATATATTTATATAAAATTAG  
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

**FIGURE 68**

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSSSTSSSDGNLRPEAITAIIVVFS  
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

**Important features:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 56-80

**N-glycosylation site.**

amino acids 36-40

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

**Tyrosine kinase phosphorylation site.**

amino acids 86-94

**N-myristoylation sites.**

amino acids 7-13, 26-32



**FIGURE 69**

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTTCAGAGGTTTTGTTTTCTTCTAGTTCTGTGCCTGCTGCACCAG  
 TCAAATACCTTCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA  
 GATGAAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA  
 TTTTTTTTCAAAATGTATCTATTAATTCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAACATGAA  
 AACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCATACACCAAGCAGTTTACA  
 GAATGTGGAGAGAAAGGCCAATACATTCACTTCACCCCTGACCTTCTACTTGGAAAAAACAAAATGAATATGGACCA  
 CCAGGCCAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTTTGATGAGTACATGAAGATCAGCCTTTC  
 TACCGTGCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAAGTGT  
 CAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACGTATGGAAAAAGATTGTCAATTCTTT  
 CCTGATAAAGTACAAACGAAAAAGCATCCATAATGTTTATGCAAAGTATTGATTCTGTTGTTGAATTTGTAAACGAA  
 AAAACCCATAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGCAATTTAGAAGTACATGGGAGGTGATTAGCAAT  
 TCTGAGGATTTTAAAAACACCATACCCATGGTGACACCACCTTCTCCACCTGTCTTCTCATTTGCTGAAGATCAGTCAA  
 AGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAAGACCGCCTAAATCGAATGAATCAAGCAGCA  
 AAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTA  
 AATAAGCTAATCCAAATAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCTCTGGGAGGA  
 ACTTCCATCTGCTCTGGAATTAATATGCATTTCAAGGTGATTGGAGAGCTACATTCCTCACTCGATGGATCCGAAGTA  
 CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTTCTTGATTGATGAAGTGAACAAAAGTGGGGCCATTGTTCTAT  
 TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTT  
 TCAGATGAAGCTCAGAACAAATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAAAG  
 TCCCTTCAGCTCGAAAGTAAGGATTAACTGTAATAGTAATGCCTGGATGAACGACACTGTCATAATTGATAGTACA  
 GTGGGAAGGACACGTTCTTTCTCATCACATGGAACAGTCTGCCTCCAGTATTTCTCTCTGGGATCCAGTGGAACA  
 ATAATGGAAAATTTACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCAGGAACTGCAAGGTGGGCACT  
 TGGGCATACAAATCTCAAGCCAAAGCGAACCAGAAACATTAACTATTACAGTAACTTCTCGAGCAGCAAAATCTTCT  
 GTGCCTCCAATCAGAGTGAATGCTAAATGAATAAGGACGTAACAGTTTCCCGAGCCCAATGATTGTTTACGAGAA  
 ATTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT  
 TTGGAACCTTTGGATAATGGTGACGGCGCTGATTCTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT  
 ACAGAAAATGGCAGATATAGCTTAAAGTTCTGGGCTCATGGAGGAGCAAACTGCGCAGGCTAAATATACGGCTCCCA  
 CTGAATAGAGCCGCGTACATACCAGGCTGGGTAGTGAACGGGGAAATTGAAGCAAAACCCGCCAAGCTTGAATTTGAT  
 GAGGATACTCAGACCACCTTGGAGGATTTGAGCCGAACAGCATCCGGAGGTGCATTTGTGGTATCACAAGTCCCAAGC  
 CTTCCTTGCCTGACCAATACCCACCAAGTCAAATCAGACCTTGATGCCACAGTTCATGAGGATAAGATTATTCTT  
 ACATGGACAGCACCAGGAGATAATTTGATGTTGGAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATTCTT  
 GATCTAAGAGACAGTTTGTGATGCTCTTCAAGTAAATACTACTGATCTGTCACCAAGGAGGCCAACTCCAAGGAA  
 AGCTTTGCATTTAAACGAGAAAATATCTCAGAAGAAAATGCAACCCACATATTATTGCCATTAAAGTATAGATAAA  
 AGCAATTTGACATCAAAAGTATCCAACTTGCACAAGTAACTTTGTTTATCCCTCAAGCAAAATCCTGATGACATTGAT  
 CCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAATCTGGAGTTAATATTCTACGCTGGTATTG  
 TCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTAAGTACCACCATTTGAACCTTAACGAAGAAAAAATCTTC  
 AAGTAGACCTAGAAGAGAGTTTTTAAAAAACAAAACATGTAAGTAAAGGATATTCTGAATCTTAAATTCATCCCAT  
 GTGTGATCATAACTCATAAAAATAATTTAAGATGTCGAAAAGGATACTTTGATTAAATAAAACACTCATGGATA  
 TGTA AAAAAGTCAAGATTAAAAATTAATAGTTTCAATTTATTTGTTATTTTATTTGTAAGAAATAGTGATGAACAAAG  
 ATCCTTTTTCATACTGATACCTGGTTGTATATTATTTGATGCAACAGTTTCTGAAATGATATTTCAAATTCATCAA  
 GAAATTAATCATCTATCTGAGTAGTCAAATACAAGTAAAGGAGAGCAAAATAAACACATTTGGAAAAAATAAAAA  
 AA

**FIGURE 70**

MGLFRGFVFLVLCLLHQSNSTFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTYLFE  
 ATEKRFFFKNVSLIPENWKENPOYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY  
 IHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISGRN  
 RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFQSIDSVVEFCNEKTHNQEAP  
 SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLVLDKSGSMGGKDRNLN  
 MNQAAKHFLLOTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK  
 YAFQVIGELHSQLDGSEVLLLTGDEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG  
 SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL  
 ITWNSLPSSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR  
 AANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA  
 GADSFKNDBGVYSRYFTAYTENGRYSLKVRAGGANTARLKLRLPLNRAAYIPGWVNGEIEANPP  
 RPEIDEDTQTTLDEFSTRASGGAFVVSQVPSLPLPDQYPPSQITDLATVHEDKIIILTWTAPGDN  
 FDVGKQRYIIRISASILDRLDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAI  
 KSIDKSNLTSKVSNIQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVI  
 VNFILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**
 amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

**FIGURE 71**

CTCCTTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAGACCATACGTCCCCGGGCGAGGGGTGA  
CAACAGGTGTATCTTTTGTATCTCGTGTGGCTGCCTTCTTATTTCAAGGAAAGACGCCAAGGTAATTTGACCCA  
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCCAGTTATGCCAGGATTTACTAGAGAGTGTCA  
ACTCAACAGCAAGCGGCTCCTTCGGCTTAACCTTGTGGTTGGAGGAGAGAACCTTGTGGGGCTGCGTTCTCTTAGCA  
GTGCTCAGAAGTGACTTGCCTGAGGGTGGACCAGAAGAAAGGATCCCTCTTGCTGTTGGCTGCACATCAGGAA  
GGCTGTGATGGGAATGAAGGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCTTTAA  
AGTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC  
CGGGGGCCCCAAACGCATGCTTCCTGTGGTCTAGCCAGGGAAGCCCTTCCGTGGGGGCCCGGCTTTGAGGGATGCC  
ACCGGTTCTGGACGCATGGCTGATTCCTGAATGATGATGGTTCCGGGGGGCTGCTTGCCTGGATTTCCCGGTTGGTG  
GTTTTGCTGGTCTCCTCTGCTGTCTATCTCTGCTGTACATGTTGGCTGCACCCCAAGGAGGACGAGGAGCAG  
CTGGCCTGCCAGGGCCAACAGCCCAAGGGGAAGGAGGGGTACCAGGCCCTCCTTCAGGAGTGGGAGGAGCAGCAC  
CGCAACTACGTGAGCAGCTGAAGCGGCAGATCCACAGCTCAAGGAGGAGTGCAGGAGAGGAGTGCAGCTCAGG  
AATGGGCGAGTACCAAGCCAGCGATGCTGCTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTC  
TGGCCCTTCTGCACTCGCAGGTGGCAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGAGTG  
CCTTTGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCCTACCCGCCACCCCGAGGAGAAGCCTGTG  
AGGAAGGACAAGCGGGATGAGTTGGTGGAGCCATTGAATCAGCCTTGGAGACCTGAACAATCCTGCAGAGAAGCAGC  
CGCAATCACCGTCTTACACGGCCTCTGATTTATAGAAGGGATCTACCGAACAGAAAGGGACAAAGGACATTGTAT  
GAGCTCACCTTCAAAGGGGACCAAAACAGGAATCAAACGGCTCATCTTATTCGACCATTCAGCCCCATCATGAAA  
GTGAAAAATGAAAAGCTCAACATGGCCACACGCTTATCAATGTTATCGTGCCTTAGCAAAAAGGGTGGACAAGTTC  
CGGCAGTTCATGCAGAAATTCAGGGAGATGTGCAATGAGCAGGATGGGAGAGTCCATCTACTGTTGTTTACTTTGGG  
AAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAACACTTCCAAAGCTGCCAACTTCAGGAACCTTACCTTCATC  
CAGCTGAATGGAGAAATTTCTCGGGGAAAGGGAATGATGTTGGAGCCGCTTCTGGAAGGGAAGCAACGCTTCTC  
TTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAG  
GTATTTTATCCAGTCTTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAA  
CAGCAGCTGGTCATAAAGAAGGAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTGATATCGGTTCAGAC  
TTTATCAATATAGGTGGGTTTGTCTGGACATCAAAGGCTGGGGCGAGAGGATGTGCACCTTTATCGCAAGTATCTC  
CAGCAGAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG  
CTGACCCCCGAGCAGTACAAGATGTGATGCACTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTG  
GTGTTCAAGCCAGAGATAGAGGCTCACCTTCGCAACAGAAACAGAAAGACAAGTAGCAAAAAACATGAACCTCCAGA  
GAAGGATTGTGGGAGACACTTTTCTTCTCTTTTGCAATTAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA  
GGACGACAAAAGAAATGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGTTGGGCTTTTACAAAGAG  
AATCAAAATCTCCGCTTTGCCTGCAAAAGTAACCCAGTTGCACCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTG  
AGATTATAAGCCTAATGGTGTGGAGGTTTGTGGTGTTTACAATACACTGAGACCTGTTGTTTGTGTGCTCATTGA  
AATATTCTATGATTTAAGAGCAGTTTGTAAAAAATTCATTAGCATGAAAGGCCAAGCATATTTCTCCTCATATGAATGA  
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAATATCAGAAAGGCAGGAGAGGATAGGCTTATATGATACT  
AGTGAGTACATTAAGTAAAAATAAATGGACCAGAAAAGAAAAGAACCATAAATATCGTGTATATTTTCCCAAGAT  
TAACCAAAAATAATCTGCTTATCTTTTGGTGTCTCTTTAACTGTCTCCGTTTCTTTTATTTAAAAATGCAT  
TTTTTCTCCTTGTGAGTTATAGTCTGCTTATTTAATTACCCTTTGCAAGCCTTACAGAGAGCACAAGTTGGCCTAC  
ATTTTATATTTTAAAGAGATACCTTGGATGATTTGATGAGAACTTTCACTTCAAAGCATCAATTTGATGCCATAT  
CCAAGGACATGCCAAATGCTGATTCTGTGAGGCACTGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTGTACT  
AATACAGACGTACAGATACTTTCTCTGAAGAGTATTTTGAAGAGGAGCACTGAACACTGGAGGAAAAAGAAATGAC  
ACTTCTGCTTTACAGAAAAGGAACTCATTGAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCATTTT  
CTCCTCAGAAGTAGGACCGCTTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACAACTCTCTTTT  
AAAACAGGGTGTCTCCTGGCTTCTGGCTTCCATAAGAAAGAAATGGAGAAAAATATATATATATATATATATTTGT  
GAAAGATCAATCCATCTGCCAGAACTAGTGGGATGGAAGTTTGTGCTACATGTTATCCACCCAGGGCCAGGTGGAAG  
TAAGTGAATATTTTAAATTAAGCAGTCTACTCAATCACCAGATGCTTCTGAAAATTGCATTTATATACCATTT  
CAAATATTTTAAAAATAAATACAGTTAATACAGTGGTTTCTTCTCATGTGAAAATTATTAGCCAGCAGCAG  
ATGCATGAGCTAATTTCTCTTTGAGTCTTCTGCTTGTGCTCAGAGTAACTCATTGTTTAAAGCTTCAAGAAC  
ATTCAAGCTGTTGGTGTGTTAAAAATGCATGTATTGATTGTACTGGTAGTTTATGAAATTAATTAACACAGG  
CCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

**FIGURE 72**

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEW  
 EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK  
 AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNNPA  
 ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKLNMAN  
 TLINIVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF  
 TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNTQPGKKVFYPVLFSQY  
 NPGIYGHHDVAPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYR  
 KYLHSNLIVVRTPVRLFHLWHEKRCMDLTPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHL  
 RKQKQKTSSKKT

**Important features:****Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 315-319, 324-328

**N-myristoylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

**Amidation site.**

amino acids 377-381



**FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPLPALQ  
 PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSGPGSEHQINSEAT  
 FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAIEHILSHLHEVRHKDQKTSVPP  
 FNLRELLPKQLGQYFRYNGSLTTPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV  
 QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
 VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

**FIGURE 75**

TGCCGCTGCCGCCGCTGCTGCTGTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGTGTC  
 TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA  
 ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACA  
 ATTGCCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGCTCCTGACAGCTCC  
 AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCTGA  
 AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC  
 ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTTCGTCCC  
 AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT  
 CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTT  
 TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT  
 GATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTTGTGCCTGCTGAAAAAATCGTGATTA  
 ACTTTATCACCCCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA  
 AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA  
 GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAG  
 AAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCGGATAAA  
 ACAGTCATTGAATATGAATATGATGTCAGAACCCTGACATTTGTGCGGGGCTGAAGAGCAGGA  
 GCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG  
 TCTTGGGCCCCGAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCG  
 CAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTTCGACTGGGA  
 TCCCCAACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTAGAGGGCTGCG  
 AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT  
 CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATA  
 TGTGCAGATGGAAAACTGATGCCAACACTTCCTTTTGCCTTTTGTTTCCTGTGCAACAAGTGAG  
 TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTTCAGTGT  
 CTGTGAGAATTACTTATTTCTTTTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA  
 GGTCTCTTAACAATGATGGTGGGCCCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAA  
 AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTTCAGGTGGGTGT

**FIGURE 76**

MSYNGLHQRVFKELKLLTLCSISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNFDRFFVPAEK  
IVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPDKTVIEYEDVRTTDICAGPEEQELSLQEEVSTQGTLLSQ  
ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDS  
EGCEPSEGDLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426



**FIGURE 77**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC  
 CTGGGAAGATGGCCGGCCCGTGACCTTCACCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC  
 CAAGCCACCCTCAGTCCCACCTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC  
 ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC  
 GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCCTGAAGCACATC  
 ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA  
 GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA  
 TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC  
 CCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTCTGTGA  
 TAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGCAGGTCATGAACCTCCTAGTGCCATCCCTGC  
 CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC  
 CTCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTGA  
 TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA  
 AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCTTGACAATGCCACCCTGGACAACATCCCG  
 TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA  
 ATTCATGGTCCTGTTGGACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC  
 TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC  
 ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTT  
 TCCCTCCAGTGAAGCCCTCCGCCCTTGTTCACCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT  
 TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG  
 ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA  
 CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG  
 CCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC  
 TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG  
 GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTG  
 CCTGTGAAAAA

## FIGURE 78

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAMREK  
PAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPATKGDTIQLYLGAKLLDSQGKVT  
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVLPESAHLKSSIGLIN  
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPLFTLGIEASSEAQFYT  
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG  
FEAAESSLTkdalvltpaslwkpspsvsq

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

**FIGURE 79**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
 TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT  
 CTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT  
 GCTGCTCCCCAGCTGGAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT  
 CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC  
 ACCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTGCAAT  
 CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC  
 GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGAGGCCTCCTGGGATTC  
 ATTCTGTGTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAG  
 CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTCTTCCCTGTTCTCCCTGATAG  
 CTGGAATCATCCTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACCTACTACGATGCCTAC  
 CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA  
 GTTCAATTCCTACAGCCTGACAGGTATGTGTGAAAGAACCAGGGGCCAGAGCTGGGGGTGGCTG  
 GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCCTGGATCGT  
 GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG  
 GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC  
 TCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCCCTCAACTTGAAACCCATTCCCTTAAGCCA  
 GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA  
 TCCCACTGACTGACCCTCTGTGATCAAAGACCCCTCTCTGCGCTGAGGTTGGCTCTTAGCTCATT  
 GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC  
 CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCA  
 GACTAATTTGTGCATGAACTGAAATAAAACCATCTACGGTATCCAGGGAACAGAAAGCAGGATG  
 CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

**FIGURE 8o**

MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMTSSAIISSSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAVNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSSLFSLIAGIILCFSCSSQRNRSNYY  
DAYQAQPLATRSSPRPGQPPKVKSEFNYSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

**FIGURE 81**

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTT  
 CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCTGCCCCCTTTCTTCT  
 GCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG  
 GTTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCTCCCGACTCCGCTCCCGG  
 ACCAGCGGCCTGACCCTGGGGAAGGAATGGTTCCCAGGTGAGGGTCTCTCCTCCTTGCTGGGA  
 CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT  
 CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCTACTTGGAGCCACAAGGCCTGATGT  
 ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCTCCACTGTCCGCT  
 GTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC  
 TCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAAACGGGACCATGTACCAACACGGAG  
 AGATCTTCAGTGCCCATGAGCTGTCCCCCTCCCGCCTGCCCAACCAAGTGTGTCTCTGCACTGC  
 ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAAGGCTGCCAGCACCCCTCCC  
 ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACA  
 GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG  
 AGAGGCCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT  
 CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCT  
 GTGTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC  
 CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
 CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGG  
 ACAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCGGGCCGGGTC  
 CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACTGCGTCGCTTTGCCCTGGAACACGAGGC  
 CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG  
 GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG  
 GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCACGAAGTCACT  
 GGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG  
 ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTGTTATTATATATTAATAAA  
 TAAGAAGTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE  
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHEL F  
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HPQDPCSSDAGRKRGPPTPAPTGLSAPLSFI PRHFRPKGAGSTTVKIVLKEKHKKACVHG GKTY S  
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQ RVTCPT EYPCRHPK VAGKCKICPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPSPDNLR RFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLDSDQESQEARLPERGTALPTARWP PRRSLERLPSPDPGAEGHQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

**FIGURE 83**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGGCCCTCCGCTCACGCAGAGCCTCTCC  
 GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCATCCGTCACCTCTCCTGTCA  
 TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC  
 TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAG  
 GACGCAGCATTCTCCTGTTTCTCTCTCCTAAGACCAATGCAGAGGCCATGGAAAGTCCGTTCTTCAGGGG  
 CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATC  
 AAGGCAGGACAAAACCTGGTGAAGGATCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAACATTACT  
 GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT  
 ACAGGTGTGAGCACTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTTGATAGAGACATCCAGCTAC  
 TCTGTCACTCCTCGGGCTGGTTCCCCCGCCACAGCGAAGTGGAAGGTCCACAAGGACAGGATTTGTCC  
 ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAA  
 CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG  
 GAGATACCTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA  
 TTTTGGGATTGTTGGACTGAAGATTTTCTTCTCCAAATCCAGTGGAATAATCCAGGCGGAATCTGGACTG  
 GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCGCGGAAACACGCAGTGAGGTGACTCTGGATCCAG  
 AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCATAGAAAAGCTCCCCAGGAGGTG  
 CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAAACATTA  
 CTGGGAGGTGACGGAGGACACAATAAAAGGTGGCGGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA  
 AGGAGTACGTGACTTTGTCTCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTT  
 ACATTAAATCCCCGTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTA  
 TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGTTTG  
 AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTTATAATGAGCAAAATGGAATCCCATAGTCATCTGC  
 CCAGTCACCCAGGAATCAGAGAAAGAGGCCCTTGGCAAAGGGCCTCTGCAATCCAGAGACAAGCAACAG  
 TGAGTCCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT  
 TCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTTCCA  
 GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTGCTGGCTGCCCTGAGCTGGGAGGGAAGAAGG  
 CTGACATTACATTTAGTTTGTCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAG  
 AACCGTCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG  
 ATCTTATTGATGACAGAGTGTATCCTAATGGTTGTTCATTATATTACACTTTTCAGTAAAAAA

**FIGURE 84**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH  
LYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYQKAIWELQ  
VSALGSVPLISITGYVDRDIQLLCQSSGWFP RP TAKWKGPQGDLSTDSRTNRDMHGLFDVEISL  
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAE LDWRRKHGQAE LR DARKHAVEVT LDPETAHPKLCVSDLKTVTHR KAPQEVPHSEKRF  
TRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVC RDDVD RRKEYVTLS PDHGYWVLR LN GEHLYFT  
LNPRFISVFPRT PPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAI PETS NSSESSQATT PFLPRGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255



**FIGURE 85**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCCT  
 GCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTCCGTGA  
 CGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCTACCCCTCGCATGGCTGGATT  
 TACCTTGGCCAGTAGTTTCATGGCTACTGGTTCCGGAAGGGGCCAATACAGACCAGGATGCTCC  
 AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG  
 GGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA  
 TACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA  
 TGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCAGGCACCCTGGAGTCCGGCTGCCCCC  
 AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCTGGATA  
 GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCTCATCCACA  
 GCCCCAGGACCATGGCACCAGCCTCACCTGTCAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA  
 ACAAGACCGTCCATCTCAACGTGTCTACCCGCTCAGAACTTGACCATGACTGTCTTCCAAGGA  
 GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCT  
 GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA  
 GAGGCCTGACCCTGTGCCCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC  
 CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCT  
 GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGAAGTCAAGGGGTGGTTCGGGGGAGCTGGAG  
 CCACAGCCCTGGTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAA  
 TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTC  
 AGCCTCTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAG  
 CTTCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG  
 AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG  
ATGAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGAGAAGTCA  
 GAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG  
 TGCAGAGTGAAAAGCACACAGGCTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCC  
 TCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

**FIGURE 86**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGYWFREG  
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY  
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTTPMISWIGTSVSPDPSTTRS  
SVLTLIPQPQDHGTS LTCQVTFPGASVTTNKTVHLNVSYPPQNLMTVFGDGTVSTVLGNGSSL  
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP  
LGSQQVYLNVSLSKATSGVTQGVVGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDGTGIE  
DANAVRGASASQGPLEPWAEDSPPDQPPPASARSSVGEDELQYASLSFQMKPWDSRGQEATDTE  
YSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

**FIGURE 87**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC  
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC  
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT  
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTGA  
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG  
GGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG  
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC  
CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT  
GTTTGGCATCTACCAGAAATATCCAGTGAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC  
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTTATTACTACCCCTAT  
GGCCAGCGGAATTCAGTGCGGGATTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA  
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
GATACTTTCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT  
GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG  
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA  
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA  
AAAAAA

**FIGURE 88**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAT  
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWTDNGPVI PVVYDFGDAQKTASYSPYGGQREFTAGFVQFRVFNNERAAALCAGMRVTGCN  
TEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSRSSREITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristoylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

**FIGURE 89**

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCCTGAACTTCCAGCCTCAGAGAC  
CGCCGCCCTTGTCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACG  
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG  
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTAGCTGGTGGCCGCGCTCT  
CTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGAGTCTCCATGTTCAAC  
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTTCAT  
ATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCTTCTGCAGTGGCCCTCCAGCTG  
TCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCTTCGATTACCTTCA  
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCTGGAAGAAGGAAG  
GCATAGGCTTCGGTTTTCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG  
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACA  
TTAAGACTTATATACAGTTTTAGGGGACAATTAATAAAAAAAAAA

**FIGURE 90**

MGRVSGLVPSRFLTLLAHLVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVSMENSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFV  
TVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

**FIGURE 91**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC  
 TCGCTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG  
 GTCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT  
 CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCTAGGGCTGCT  
 GGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCGAACCACAGCCCCC  
 CACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG  
 GCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT  
 CCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG  
 AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG  
 GAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG  
 CTCCCAGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTG  
 TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTAC  
 CATAGTGATACCCCCTACTACCCATCTGGGTTGACCCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC  
 TGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTC  
 AGGCAGGGAGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG  
 AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTACTAGATCACAGGAGCACTGG  
 AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG  
 TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC  
 CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA  
 GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCTAGGAGCCAGTCAGCAGGGTGGGGTGGG  
 GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATGG  
 CATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC  
 CAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG  
 GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC  
 CGCGTGTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG  
 GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACACGGGGTCTCCCGGATCTGGATGGCGC  
 CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCGGGCCGAGAGCATGTGCTGGATCTGTTC  
 TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT  
 TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

**FIGURE 92**

MLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF  
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDP  
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71



**FIGURE 93**

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCC  
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTT  
CTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAA  
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAAACC  
AGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTTGGAATCATGA  
GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTAT  
GGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT  
ATTCTGGGGCATTGTATTTTTTGTATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC  
TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG  
TCAGCATTTATAATCCTGGTGCTCATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG  
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTCTTTACAACCAGCGCTCCAGAT  
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT  
TTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

**FIGURE 94**

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLT  
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKNFLLYNQRSR

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

**FIGURE 95**

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTCGTG  
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGGATCAAC  
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTCCGGATCAGG  
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAACA  
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTAAATCCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTTGTACACAACCTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC  
TTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCATCCTGCCACCAGTCAGGCAGGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG  
GAACCCAGCAGGCCGCCTCCCAACTCCCAGTGGCACAGATGACGACTTTGCAGTGACCACCCCT  
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA  
GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT  
TACCTGAAAATATTCTTGAAATTTTCAAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA  
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT  
TAAACATATTTGGAAAAC TGAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQSNQVFPSLSLIPLTQM  
 LTLGPDHLHLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
 LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
 TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

**FIGURE 97**

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT  
 CTTCTTGCTTGCCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCTGTCTTGACCATG  
 GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGCCCAGCCTGC  
 AGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAATTTCCCTTTATACCTGACCAAGTTGC  
 CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCAGGCAAGGCAACTGAG  
 GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTGACCAGGGCCCTGGACCGAGAGGA  
 GCAGGCAGAGTACCAGCTACAGGTCACCCCTGGAGATGCAGGATGGACATGTCTTGTTGGGGTCCAC  
 AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCATTTCTCTCAAGCCATCTAC  
 AGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCCCCTTCTCTTCTTGAGGCTTCAGACCG  
 GGATGAGCCAGGCACAGCCAACCTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCAGC  
 CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC  
 ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA  
 CCAGGCCTCAGGCCACCAGGCCACTGCCACCGTGGAAGTCTCCATCATAGAGACACCTGGGTGT  
 CCTTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTTATACCCGCACCACATGGCCAGGTA  
 CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCCGGGACCTTTGAAGTGAA  
 TGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCC  
 AGGTGCGGGCTCAGAATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTG  
 ATGGATGAGAATGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCTGAGCT  
 CAGTCCACCAGGTACTGAAGTGACTAGACTGTGACGAGAGGATGCAGATGCCCCCGGCTCCCCCA  
 ATTCACCGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC  
 CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT  
 CCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCACACGTGTGAAG  
 TCGAAGTCGAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCCAGATTGGGCCT  
 ATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA  
 CCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTG  
 GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG  
 GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCCC  
 AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGAGAGAGATGATGCCACCCCCAAGTTGG  
 ACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCCAGCCGGCTCTTCTCTGCTGACCATC  
 CAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT  
 CTGCATTGAGAAATTTCCGCGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG  
 ACACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA  
 TACCTTGACACACCCCGCCAAGACCATGGCTTGATCGTGAGTGAGCCAGCAAGGACCCGATCT  
 GGCCAGTGGGCACGGTCCCTACAGCTTACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGC  
 GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGT  
 GAACACATAATCCCCGTGGTGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGAT  
 CGTGTGTGCTGCAACGTGGAGGGGAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCCA  
 CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCTGGTAGCAATAGGAATCTTCTCATCCTC  
 ATTTTCACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCT  
 GAAGGCGACTGTCTGAATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG  
 TCCCCCTGGGAGAGAGCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCTCCA  
 TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCACTT  
 TATGGACTGCCCATGGGAGTGCTCCAAATGTGAGGGTGTGTTGCCCAATAATAAGCCCCAGAGAA  
 CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

## FIGURE 98

MVPAWLWLLCVSPQALPKAQPALSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT  
 EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI  
 YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG  
 STSLDHALERTYQLLVQVKMDGQASGHQATATVEVSI IESTWVSLEPIHLAENLKVLYPHHMAQ  
 VHWSSGDVHYHLESHPPGPFVEVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL  
 VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSHVYQLLSPEPEDGVEGRA  
 FQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIG  
 PISLPEDVEPGTLVAMLTAIDADLEPAFRLMDFAIERGDTEGTFGLDWEPPDSGHVRLRLCKNLSY  
 EAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPI SAPAGSFLLT  
 IQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALT LAPVPS  
 QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGNPTVQRDWRLQTLNGSHAYLTLALHWVEP  
 REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTTLVAIGIFLI  
 LIFTHWTMSRKKDPDQPADSVPLKATV

### Signal peptide:

amino acids 1-18

### Transmembrane domain:

amino acids 762-784

**FIGURE 99**

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGCCTG  
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA  
TCTCTTACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTAC  
ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG  
TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTTCCAATGAGACTAGCACC  
TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG  
TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA  
GCATAGTCACCAACTCTGAGTTCCATACACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG  
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCCACCACT  
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC  
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT  
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCA  
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG  
TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCCACCAATTCTGAGTCCAGCACACCTCC  
AGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCAC  
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA  
GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA  
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA  
ATGCACACAACTTCCCATAGTGCATCTACTGCAGTGTGAGGCAAAGCCTGGTGGGTCCCTGGT  
GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGC  
TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCT  
CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCACAGGCCAG  
GTGGAGTCCTAACTGGTTCTGGAGGAGACAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA  
ACAGCGGGCCCCTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCA  
CCCAAGACCTGGTTTCTTTTATTTCATCCCAGGAGACCCCTCCAGCTTTGTTTGGATCCTGAA  
AATCTTGAAGAAGGTATTCCTCACCTTTCTTGCCTTTACCAGACACTGGAAGAGAATACTATAT  
TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTG  
CCCCGGGTGGGTATCTAGCTCTGAGATGAACTCAGTTATAGGAGAAAACCTCCATGCTGGACTC  
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS  
 SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS  
 GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA  
 TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES  
 STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS  
 GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
 TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESSTVSSGISTVTNSES  
 STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA  
 AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRPVSII  
 AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532



**FIGURE 101**

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA  
 CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTGACAGGTG  
 GGAGGCTGGAACATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT  
 GGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT  
 AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT  
 GGTGTCATGGAAAGGATTTACTTTATACTGACTCTGTTTTGGGGAAGCTTTTTTGGGAAGCATTT  
 TCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATCGCTGGATCAACAAC  
 CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAAAGT  
 GATTATAACTGGGGATGCATTTGTTCCCTGGAGAAAGAAGTGTCATTATCATGAACCATCGGACAA  
 GAATGGACTGGATGTTCCCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAAATT  
 TGCCTCAAAGCGAGTCTCAAAGGTGTTCCCTGGATTGTTGGGCCATGCAGGCTGCTGCCTATAT  
 CTTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTGGAAGACATGATTGATTACTTTTGTG  
 ATATTACGAACCACTTCAACTCCTCATATTCCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
 TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG  
 AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCCTTGATGCTGTCCATG  
 ATATCACTGTGGCGTATCCTCACAACTTCCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT  
 CCCAGGGAATCCACTTTCACGTCCACCGGTATCCAATAGACACCCCTCCCCACATCCAAGGAGGA  
 CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAG  
 GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCATTCCACCTTGCAAGTCTGAACTCAGGGTC  
 CTTGTGGTCAAATTGCTCTCTATACTGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCAT  
 ATATTTGTACAGTCTTGTAAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA  
 GAATATTTGGTGGACTGGAGATCATAGAACTTGTCATGTTACCGACTTTTACACAAACAGCCACAT  
 TTAAATTCAAAGAAAAATGAGTTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTG  
 GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTCATGACTATGTGCAATATTTCTTACT  
 GCCATCATTATTTGTTAAAGATATTTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTTT  
 TTTAATCTCTGAATGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT  
 GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAAA

## **FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFSGIMVSWKGIYFILTLFWGSFFGSI FMLS P  
 FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
 FLWNCLMRYSYLRLEKICLKASLKGVPFGWAMQAAAYIFIHRKWDDKSHFEDMIDYFCDIHEP  
 LQLLIFPEGTDLTENSKSRNAFAEKNGLOKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA  
 YPHNIPQSEKHLQGDFFPREIH FHVHRYPIDTLPTSKEDQLWCHKRWEEKEERLSFYQGEKNF  
 YFTGQSVIPPCKSELRVLVVKLLSILYWTLESPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG  
 LEIIEIACRYRLHKKPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

**FIGURE 103**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC  
 TCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTTCATAGTGTGAGATCAACCCACAGGAATA  
 TCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT  
 CACTGGACCGGCAAGTTTGTCCAGGCCCTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT  
 TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAGTTCCATGCTGTGGTC  
 CACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAAGTGA  
 GTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTAAGGCTAAAAACATCACTCCCTCGG  
 ACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCAGATTTACGATGAGGAGGCCACCTGGGAGCTG  
 CGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCATCGTGGGATATGTTGACGGAGGTATCCA  
 GTTACTCTGCCTGTCCTCAGGCTGGTTCCCCCAGCCACAGCCAAGTGGAAAGGTCCACAAGGAC  
 AGGATTTGTCTTCAGACTCCAGAGCAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC  
 ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA  
 GGTGGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTA  
 TTTTACTCGGGTTACTCTGTGGTGCCTGTGTGGTGTGTCATGGGGATGATAATTGTTTTCTTC  
 AAATCCAAAGGGAAAATCCAGGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG  
 AGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG  
 TTTCTGATCTGAAAATGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCCTCACTCTGAGAAGAGA  
 TTTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA  
 CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACA  
 ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTT  
 ACATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCTACACGAGTAGGGGTCTTCTT  
 GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCTTGC  
 TGACATGTGAGTTTGAAGGCTTGTGAGACCTATATCCAGCATGCGATGTATGACGAGGAAAAG  
 GGGACTCCCATATTCATATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCCTGCTTAAAGGGC  
 CCCACACCACAGACCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCTCT  
 CCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTAGGGAGCTGAGGTTCTTCTGCCC  
 TGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAG  
 TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA  
 CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTTGCTAGTCACGG  
 ACAGTGATTCTGCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGACAGGT  
 TGAGGGCACAGTGTGCTAATGATGTGTTTTTATATTATACATTTTCCACCATAAATCTGTT  
 TGCTTATTCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACC  
 TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTTTCACTGATTCTATAAGCCCAGCAT  
 TACCTGATACCAAACAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCC  
 CTCATTAACACAGACACAAAAATTTAAATAAAATTTTAAACAAATTAACATAAACAATATATTTA  
 AAGATGATATATAACTACTCAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTAATATTTAAAT  
 ATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAGAAAACCATAAAAA

**FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH  
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGDLSSDSRANADGYSLYDVEISI  
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALCGVVMGMIIVFFK  
SKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPQEVPHSEKRF  
TRKSVVASQGQAGRHYWEVDVGQNVGWYVGVCRRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT  
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLCQFEGLLRPYIQHAMYDEEKG  
TPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

**FIGURE 105**

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG  
 TTTGTTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCCTGGCAGTGTGCATTGGA  
 CTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAATTACTATAGCACATTGTCATTTACAAC  
 TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAAATTTTACAGAAATGAGCCAGAGACTTGAAT  
 CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTGTCAAGTCTCAGGTTATCAAGTTC  
 AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTGTAGATTCTACTGAGGATCCTGA  
 AACTGTAGATAAAATTTGTTCAACTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG  
 ATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA  
 ACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAAGTAGAAGAGGGTGAATG  
 GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC  
 TTGTGAGTGCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA  
 ATAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAATAATGTCCATGAAAAATACAAACCCCATCACA  
 TGACTATGATATTTCTCTGCAGAGCTTTTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTC  
 TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTGTGACAGGATTTGGAGCACTGAAAAAT  
 GATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACC  
 TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT  
 GCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG  
 AGCTGGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTGTGTTATACTAGAGTTACGGCCTTGCGGGACTG  
 GATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTTG  
 GGTGTGGAGGCCATTTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCA  
 ATAAACTGTTGCTTGATGCATGTATTTTCTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA  
 GATCAACTCTGTCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATACAATATTAC  
 ATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTTGTGAGAATTTGACTTGTGACATAAATTTGTAAT  
 GCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCTCAGCTCCTCTCATTTACAGCAATATCCATTT  
 TCAAGGTGCAGACAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAA  
 AAGTATTAGGTGTTTCTTAGTGGAATATTAGAAATGATCATATTATTATGAAAGGTCAAGCAAAGACA  
 GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACCTAAGTTAAGGAAGTCCAGAAAGAAGCCAAG  
 ATATATCCTTATTTTCATTTCCAAACAACCTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTGACCT  
 ATAAATATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATATTTATTTAACATTG  
 TTAAGGATGTCAACATATAACAATAAATATAAATCACCCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTDKLY  
 AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQOKHGVLAHMLLICRFHSTED  
 PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG  
 TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL  
 RRIIVHEKYKHPSHDYDISLAELSSPVYPYTNVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS  
 QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDGGPLVSSDARDIWYLAG  
 IVSWGDECAKPNKPGVYTRVTALRDWITSKGTI

**Transmembrane domain:**

amino acids 21-40 (type II)

**FIGURE 107**

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCTTG  
 CCCCAGATGAGCCCCGCGGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGGGCCAGC  
 GCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT  
 ACGGGGCTCACAAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTACGCCCTCAA  
 TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA  
 ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTGACTTACTTTCCT  
 GTGGTTCATCCGGTCATGATTGCTGTTTGTCTGTTTCCTTATCATTGTGGGGATGTTAGGATATTG  
 TGGAACGGTGAAAAGAAATCTGTTGCTTCTTGATGGTACTTTGGAAGTTTGCTTGCTATTTCT  
 GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATGGTTCCAGTACAATGGTCA  
 GATATGGTCACCTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA  
 TGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAGTCTGTGGAGTAGTATATTTCACTGACTGGTTGG  
 AAATGACAGAGATGGACTGGCCCCAGATTCCCTGCTGTGTTAGAGAATCCCAGGATGTTCCAAA  
 CAGGCCCCACAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTT  
 TTTGAGAGGAACCAACAACACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA  
 TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGG  
 ACAGACCAAAATGATGTCCTTGAAGAATGACAACCTCAGCACCTGTCATGTCCTCAGTAGAACT  
 GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT  
 TTGAGATGGAGGAGTTATAAAAGAAATGTCACAGAAGAAAACCAAACTTGTATTTATGGACT  
 TGTGAATTTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAA  
 TAACACCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTC  
 ACCACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC  
 TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTTGATTAGCATTTCGCA  
 TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTACTTCTACCAA  
 CTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTTATTA  
 CTCAGCGATCTATTCTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACT  
 ACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCCTTAAAAGAGCAAGCTAACACAT  
 TGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCACTCGAT  
 TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATT  
 ATTTTTAGCCTTTCCGTGTTAATAAAGCTTTACTATTCTGTCTGGGCTTATATTACACATATAAC  
 TGTTATTTAAATACCTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTC  
 AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTTCAGA  
 AAGGACTTGTATGCTGTTTTCTCCCAAATGAAGACTCTTTTGGACACTAAACACTTTTTAAAAA  
 GCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTTCTACAGAAAA  
 TAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAAACATGTGACAATTTAGAGATT  
 CTTTGTGTTTATTTCACTGATTAAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTACAA  
 GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTGTTAT  
 TTCTCAGAATATGGAAGAAAATTAATGTGTCAATAAATATTTCTAGAGAGTAA

**FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT  
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPQTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248



**FIGURE 109**

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTCTCTGATAAAGCCCTACCAGTGCT  
 GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA  
 CCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTCCAGAAGGATGCCTCCATTCTGCTTCTCACCTG  
 CCTCTTCATCACAGGCACCTCCGTGTCACCCGTGGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGC  
 CCTGGAGGAACACTGACCACCAGTTGGATGAGTCTCAAGGTCTCCTCTATGTGACAACCATGTGAATGGGGAG  
 TGGTACCACTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA  
 CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAAGGCACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT  
 TCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGAAGTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT  
 CTGACCAAGCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTATGACATCTGCGACGAGGACTGCCATGG  
 CAGCTGCTCAGATACCAGCGAGTGCACATGCGCTCCAGGAAGTGTGCTAGGCCCTGACAGGCAGACATGCTTTG  
 ATGAAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCGCTGT  
 GAGTGTGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA  
 TGGTGGCTGCAGCCACTCTTGCCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCGGGGCTGGTGTGT  
 CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAATCAAATGCCATTGAAGTGAACATCCCAGGGAG  
 CTGGTTGGTGGCTGGAGCTCTTCTGACCAACACCTCCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACAT  
 CCTCTTCTCTCAAGACATGTGGTACAGTGGTGCATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA  
 CAGGTCTACCCAAGCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG  
 ACCTGCGAGTTTCCACGCCTGTACACCATTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAT  
 CATGAGCCGAAATCATGGGATCTTCCATTCACTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC  
 GGGAAAGCTCTGCCCACCCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGCACGTGAGCGGC  
 TTGGAAGCTTGGTGGAGAGCTGCTTGGCACCCCCACCTCCAAGATCGACGAGGTCTGAAATACTACCTCAT  
 CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAGCACTTCCAGG  
 TCCCTGTCTTCAAGTTTGTGGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGGTCTTGTCTGTGGAGTG  
 TTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGGCGAATGCGTCTGGGGCAGGAGGAGAGGACTCAGC  
 CGGTCTACAGGGCCAGACGCTAACAGGCGGCGCGATCCGCATCGACTGGGAGGACTAGTTCGTAGCCATACCTC  
 GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACC GCCCTTAAGAACATCTGCCAACAGC  
 TGGGTTACAGACTTCACACTGTGAGTTCAGACTCCCAGCACCACCTCACTCTGATTCTGGTCCATTCACTGGGCA  
 CAGGTACAGCACTGCTGAACAATGTGGCCTGGGTGGGGTTTCATCTTTCTAGGGTTGAAACTAACTGTCCA  
 CCCAGAAAGCACTCACCCATTTCCCTCATTTCTTTCTACACTTAAATACCTCGTGTATGGTGCAATCAGAC  
 CACAAAATCAGAACTGGGTATAATATTTCAAGTTACAAACCTAGAAAATTAACAGTTACTGAAATTATGA  
 CTTAAATACCAATGACTCCTTAAATATGTAAATTATAGTTATACCTTGAAATTTCAATTCAAATGCAGACTAA  
 TTATAGGGAATTTGGAAGTGATCAATAAACAGTATATAATTTT

**FIGURE 110**

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP  
 TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV  
 YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
 LRS DGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLSEDNHTCQVPVLCKSNAIEVNIPREL VGG  
 LELFLTNTSCRGVSN GTHVNILFSLKTCGTVVDVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
 CEFPRLYTISEGYVFNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEOPYREALPTLKL RDSLYFGIEPVVHV  
 SGL ESLVESCFATPTSKIDEVLKYILIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV  
 LVCGVLDERSRCAQGCRRMRRGAGGEDSAGLQGQTLTGGP IRIDWED

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

**Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

**N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

**ZP domain proteins.**

amino acids 431-457

**Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

**FIGURE 111**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG  
 GCCTCCTCCAGCCAGTGTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT  
 CCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT  
 TACAGGATCCTGACAGTGTATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC  
 ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATATAGCACTACTGAGCCTGGCGAGTATCATCATTGT  
 GGTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCGA  
 GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC  
 CCCGAAGGGCCTGCAGTGGCAGTCCGCCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC  
 AGGGAATGGTTCTCTGCCTGTTTCGACAATTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG  
 GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG  
 GAGCTTCGCATGCGGAACCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTG  
 TGGGAAGAGCCTGAAGACCCCCGTGTGGTGGGTGGGGAGGAGGCCCTCTGTGGATTCTTGGCCTTGGCAGG  
 TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCAGGGCA  
 GCCCCTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAG  
 CTTCCTCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACA  
 TCGCCCTCATGAAGCTGCAGTTCCTCACTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT  
 GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA  
 GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGT  
 ACCAGGGGGAAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGT  
 GACAGTGGTGGGCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG  
 CTGCGGGGGCCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT  
 GGAAGGCTGAGCTGTAATGTGCTGCCCCCTTGCAGTGCTGGGAGCCGCTTCCTTCTGCCCTGCCACCT  
 GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCCCTCTGCCCACAGCCTCAGCAT  
 TTCTTGGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCCCTCGCAGCCCAGAGCGCCAGAGGAAGTCA  
 GCAGCCCTAGCTCGGCCACACTTGGTGTCTCCAGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCT  
 CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCC  
 CAGATCACTGTGGGCTGGAGAGGAGAAGGAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA  
 GCCTACTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT  
 ACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAA  
 AAAA

**FIGURE 112**

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFLCG  
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN  
FTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL  
KTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKL  
GSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWG  
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCCQDSGGPLMYQS  
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

**FIGURE 113**

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA  
 TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCACAGGAGT  
 TGAAC TGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAATC  
 TGTTTTTTGTTCTCTTGTAAC TAGCCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT  
 GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCTTCGAAG  
 CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAACTGTCTCACGTCT  
 GGAGGCACTGACTCGGGCAGTGCAAGTAGCTGAGCCTCTTGGTAGCTGCGGCTTCAAGGTGGGC  
 CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTTTCATAGGCGATGGCTCCCACTGCC  
 AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCCGTGGACACCTGCTCA  
 GAAGCAGTGGGTGAGACATCACGCTGCCCCGCCATCTAACCTTTTCATGTCCTGCACATCACCTG  
 ATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
 CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCATTCTCTGGAACATGAGG  
 GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAAGTTGTGCCAAATTATGGGTGAGAAAAGATG  
 GAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGCATTAGTGACATGTGGGGGAAGGGCTG  
 CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT  
 CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA  
 TCTGCGATCACCAGCCAGGGGCGAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCC  
 CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG  
 GGCTAATGGCTCAGTGTGGCCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT  
 GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG  
 CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTT  
 CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCA  
 AACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT  
 TTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGG  
 TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC  
 CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA  
 GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTA  
 TGGTTATTTGTAA

**FIGURE 114**

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

**Signal peptide:**

amino acids 1-15

**FIGURE 115**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTAAATCCAAGAAA  
ATATGTAAATCACCTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCTAATTGTCCT  
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAAGCCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAAGTAAATA  
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG  
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGTGATTCTGAATTTT  
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTCTTTGAACAGTCAGTG  
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGA  
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG  
ACTTTGAGGAGGAGGAGAAGATCTTCACTTTCCTGCCAACGAAAAAAGGGATTGAACAAAAT  
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA  
AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG  
GTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA  
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTG  
TAACTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC  
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCT  
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA  
TTATCACCAAAAAAAAAAAAAAAAAAAAA

)

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTIVLFWGSKHFWPEVPKKAYDME  
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEEITTTFFEQSVIWPAPKPIENRDFLKNKILEICDNVTMYWINPTLISVSE  
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD  
ERGYCCIIYCRGRNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14



**FIGURE 117**

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA  
 GGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCTCTGTCCATCCTGGGGCT  
 GGCGGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCAGGACCTGTACGACAACCCCGTCACCT  
 CCGTGTTCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCC  
 TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCT  
 GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG  
 CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG  
 TCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG  
 GATGGTGCAGACTGTTTCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGGGCTGGTTCGCTGGAGGCC  
 TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCTGGCACCAGAAGAAACCAACTACAAA  
 GCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT  
 TGGGTCCAACACCAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC  
 CTTCGAAGCAGCACTATGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA  
 CCAAAAAACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCT  
 CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACA  
 GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTTAAATATAACT  
 TTCTACTCTGATGAGAGAATGTGGTTTAACTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC  
 TTCTCCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCCAAGAAAACTTTGAAAGGAAA  
 GAGTAGACCCAAAGATGTTATTTCTGCTGTTGAATTTGTCTCCCCACCCCAACTTGGCTAGTAATAA  
 ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT  
 ACACTGTGATCTTAAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTG  
 TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCCTTTCTGT  
 CGCGGGTCAGAAATGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTTAAGTCCTAAATATAGTTAA  
 AATAAATAATGTTTGTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG  
 GAAATGAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCC  
 ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT  
 TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA  
 TGGTGGCATAACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT  
 TGGGGCTGCAGTGAGCCATGATCACACCCTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA  
 AATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAAACTAATTCTTTAA

**FIGURE 118**

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP  
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNEWMSTANMYTGMGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY  
V

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

**FIGURE 119**

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCC  
 AGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG  
 GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTGGCCTTCATT  
 GAAAACAACATCGTGGTTTTTGAAGAACTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
 CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGCCAGAG  
 GACTGATGTGTGCTGCTTCCGTGATGTCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC  
 ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT  
 CATCACGGGCATGGTGGTGTCTATCCCTGTGAGCTGGGTGGCAATGCCATCATCAGAGATTTCTATA  
 ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCA  
 CTGGTGTGATGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTA  
 CAGATACTCGATACCTTCCCATCGCACAAACCAAAAAGTTATCACACCGGAAAGAAGTACCGAGCG  
 TCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAATG  
 AAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTTACTGTTCTTAACTGCCT  
 AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTAGCAGAAATGAGATA  
 TTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA  
 CTCTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC  
 ACGACATAGCATTATGTACATAGATGAGTGTAAACATTTATATCTCACATAGAGACATGCTTATATGGT  
 TTTATTAAAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA  
 ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCA  
 TTTATAATGAAGATTAATAATGAAGGCTTAAATCAGCATTGTAAAGGAAATTGAATGGCTTCTGATAT  
 GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT  
 CTTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTGTCAAGGGGCTTTCATTCAAACCTGCTT  
 TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGATGGTTTTAGGAAAGTG  
 AAAATATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGAT  
 ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAGAGCAGAAAAATA  
 TGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTACCT  
 GCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTGTCTGTGAAAAATAAATTTCTTCTTGTGA  
 CCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTCTGTTTATCCAAATTTGATGAA  
 ACTGACAATCCAATTTGAAAGTTTGTGTGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTT  
 TATACATTTATATTAATAAATGTACATTTTCTAATT

**FIGURE 120**

MATHALEIAGLFLGGVGMVGTVAVTVMPOWRVSAFIENNIVVFENFWEGLWMNCVRQANIRMQCK  
IYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG  
MVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY  
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

**FIGURE 121**

GGAGAGAGGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGCGGAG  
CCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAGCC  
GGGAGCCATGCGACCCCAGGGCCCCGCGCCTCCCCGAGCGGCTCCGCGGCCTCCTGCTGCTCC  
TGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAGGCGCAG  
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC  
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCGGGATG  
GATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTAC  
AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGACATT  
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTGTTCAGTGGCTCACTTCGGCTAAAATGCA  
GAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTACAGGACCTCTTCCC  
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCG  
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG  
TTGGCACTTGTTTACAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC  
ATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCC  
TTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG  
CTAAATATGTTTACAGACCAAAGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTG  
CTTCAATCAAAGTGGTTTCAATATTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT  
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTCTTTTCTCTTAGTATAGCATTTTTTA  
AAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT  
TAAATAAAAATTATTTCCAACA

## **FIGURE 122**

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAAGVPGR  
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK  
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGSLPIEAIYLDQGSPENSTINIHRTS  
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRRIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

**FIGURE 123**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA  
 CTGGGTGCTCATCACGGGAAGTGTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
 ATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTA  
 ACCGCCCCCTCCCCACCCCCCAAAAACTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC  
 TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTGTCTTGGAG  
 TGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT  
 TCTTCCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTGATGCAACTG  
 GCCCCAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG  
 TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG  
 CTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTGA  
 ATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT  
 ATAACAGCCTTCAAAAACCTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC  
 CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGA  
 GCTGATTCTTAGTTCCAATAGAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAAT  
 TACGGAACCTTGGATCTGTCTTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG  
 CGGAAGCTGCTGAGTTTACATTTACGGTCTAATCCCTGAGAACCATCCCTGTGCGAATATTCCA  
 AGACTGCCGCAACCTGGAACCTTTTGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG  
 TCTTTGCTGGCATGATCAGACTCAAAGAACCTTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC  
 CTGGCCCTTTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAAGTGAATAAAATCAGTGT  
 CATAGGACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA  
 TCGAAGCTTTTCAAGTGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCTCAACCTGGAT  
 TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG  
 TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTGTAAACTGGCTGAAAAGTT  
 TTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG  
 ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGTCTGGCCAG  
 GGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAAACCCCTT  
 TGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCT  
 TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCTGTGTTAT  
 CTACGTGTGATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA  
 GGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAATGACTCCAGCACCCAGGAATTTTATGTA  
 GATTATAAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCTGCACCTA  
 TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTGTGATAAAAAGAGCTCTTAAAAGCT  
 GGGAAATAAGTGGTGCTTTATTGAACCTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCC  
 TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCTTGTCCGTTTTAGTGCATTGATAAATCT  
 GGTCAATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT  
 GAACCTCCGGTTTAAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTGCGATT  
 GTTTTAAAGATAAACTTCTTTTCATAGGTAAAAA

**FIGURE 124**

MGFNVIRLLSGSAVALVIAPTPLLTLSSAERGCPKGCRCGKMVYCESQKLQEIPSSISAGCLG  
 LSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR  
 PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIQDCRNLELLDLGYNRIRS  
 LARNVFAGMIRLKEHLEHNQFSKLNLFRLVSLQNLVYLQWNKISVIGQTMSWTWSSLQRLDL  
 SGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIQEILDWISLNDISLAGNIWECSRNICSLVN  
 WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE  
 SKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVILLVIYVSWKRYFASMKQLQQR  
 SLMRRHRKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512



**FIGURE 125**

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGGCTTTTGCCGCTG  
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT  
AGCAACCTTTCCCTGGATCTCACAAAACCTCGACTCCAATGCAAGGAGAAGCAGCTCTTGCTC  
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC  
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT  
GTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG  
ATGAGCATTATCCCCTTTGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT  
TTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAATGGAAGGAAAAAGGAACTGGAAGG  
AAAACCATTGCGATTTCTGTGGTGTACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC  
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA  
ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC  
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA  
TCAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG  
ACTGACTGCTTGATTGAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACC  
ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCCATTTTAA

**FIGURE 126**

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES  
APYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNQF  
RDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTWPWSMVFWLTYEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

**FIGURE 127**

CGCGGATCGGACCCAAGCAGGTCGGCGGGCGGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCGAC  
 CCCC GTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCATGGCCAGGCCCGGCATGG  
 AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCGCTCGGGGGGCATCGGCGCGGCCGTGGCC  
 CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA  
 GCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCCTACAGATGTGACCTAT  
 CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC  
 TGCATCAACAATGCTGGCTTGGCCCGGCGCTGACACCCTGCTCTCAGGCAGCACCAGTGGTTGGAA  
 GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA  
 AGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTTA  
 CCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCCTGCGCTGACAGAGGGACT  
 GAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG  
 AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA  
 ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCCTCAGCACCCCCGCACA  
 CATCCAGATTGGAGACATCCAGATGAGGCCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC  
 TCCTTCCCTCCCCACCCTTCATGGCTTGCCCTCCTGCGCTCTGGATTTTAGGTGTTGATTTCTGGAT  
 CACGGGATACCACTTCCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTATA  
 TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC  
 TAATTGTTTTACTTGTTAACTTGTTCTTGTGCCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTG  
 TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTG  
 TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTACCTTATATCTGTGTTGTTATCCAGGGCTCC  
 AGACTTCTCTCTGCTGCCCCACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC  
 AGCCCAGTCTTGGCTTCTTGTCCCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG  
 CAGAACACCAGGGCCTGGCCCAGTGGATTTATGGTGATCATTAAGAAAGAAAAATCGCAACCAA  
 AAAAAAAAAA

**FIGURE 128**

MARPGMERWRDRLALVTGASGGIGA A VARALVQQGLKVVG CARTVGNIEELAAECKSAGYPGTLI  
PYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALSICTR  
EAYQSMKERNVDDGHIININSMGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

## FIGURE 129

AACCTTCTACATGGGCCTCCTGCTGCTGGTGCCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT  
 CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCGGGAGC  
 ACCTCCCTCCCAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCAGTTCTGGTTTCATGC  
 CAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA  
 GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCAATTCAGTAGCCACCAGCCACCTGTGG  
 CCGTTGAGTGCTTGAAATGAGGAACTGAGAAAATTAATTTCTCATGTATTTTTCTCATTATTTA  
 TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA  
 TATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT  
 TTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC  
 CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT  
 GCACCACAATGCCCAACTAATTTTTGTATTTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG  
 CTGGCCTTGAACTCCTGGCCTCAAACAATCCACTTGCCTCGGCCTCCCAAAGTGTATGATTACA  
 GGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTTGTGTTGGGAACTTTGAAATTAT  
 ACAATGAATTATTGTTAACTGTCTCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT  
 ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC  
 AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCACATGTG  
 AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG  
 TTCCATCCATGTTGCTGCAAATGACAGGATTTTCGTTCTTAATTTCAATTAAAATAACCACACATG  
 GCAAAAA

### **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV  
KGHGTLGESPMFPKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

**FIGURE 131**

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
 ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG  
 TCCATCTGTGTGCTGCGTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTCTGACATCCATTCACACAG  
 GAATACCAGAGGATGCTACAACCTCTCTACCTTCAGAACAACCAAATAAATAATGCTGGGATTCTTCAGAT  
 TTGAAAAACTTGCTGAAAGTAGAAAGAATATACCTATACCACAACAGTTTAGATGAATTTCCCTACCAACCT  
 CCCAAAGTATGTAAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA  
 AAATTCCTATCTGGAAGAATTACATTTAGATGACAACTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA  
 TTCCGAGACAGCAACTATCTCCGACTGCTTTTCCTGTCCCGTAATCACCTTAGCACAATTCCTGGGGTTT  
 GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCATCTCTTCAAG  
 GTCTCACTAGTCTAAAACGCTGGTTCTAGATGGAAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT  
 TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATTCCCTGACTGCTGCACCAGTAAACCT  
 TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCCAAATGCTTTTT  
 CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT  
 GATGATTTGGACAATATAACACAACCTGATTCCTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG  
 GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA  
 AGGTTGCTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGC  
 ACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCAAGGACAGTGGCCAGCTCCAGTGAC  
 CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA  
 CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTATATCTCTTGAAACTTGCTCTACCTATG  
 ACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATAGCCCGGCATTGGATCTATAACAGAAACAATTGT  
 AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTCACCCATATAAAGTATGCATGGTTC  
 CCATGGAAACCAGCAACCTCTACCTATTTGATGAAACTCCTGTTGTATTGAGACTGAAACTGCACCCCTT  
 CGAATGTACAACCCTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACC  
 TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGTATG  
 TTCATAGGAATGGATCGCTCTTCTCAAGGAAGTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
 GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAACTTCTTTTCAGATGTTACCAAT  
 AAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAATACACACCATATTTCCCTCCTAATGGAATGAATCTGT  
 ACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC  
 TCACACTCATTGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTAAACCTAAGGGAGGTGATG  
 GT

**FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCND RFLTSIPTGIPEDATTLYL  
 QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL  
 EELHLDNSVSAVSIEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL  
 QGLTSLKRVLVDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAFPVNLPGTNLRKLYLQDNHIN  
 RVPPNAFSYLRQLYRLDMSNNNLSNLPQGFDDLDNITQLILRNNPWYCGCKMKWVRDWLQSLPV  
 KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQQQWPAPVTKQPD  
 IKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET  
 IVTGERSEYLVTALEPDSPYKVCMPMETSNLVLFDETPVC IETETAPLRMYNPPTTLNREQEKE  
 PYKNPNLPAAIIGGAVALVTIALALLVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS  
 ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSESSSNRSYRDSGIPDSDHSHS

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site.**

amino acids 515-522

**N-myristoylation sites.**amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645**Amidation site.**

amino acids 567-570

**Leucine zipper pattern.**

amino acids 159-180

**Phospholipase A2 aspartic acid active site.**

amino acids 34-44



**FIGURE 133**

CCGTCATCCCCCTGCAGCCACCCCTTCCCAGAGTCCTTTGCCAGGCCACCCCAGGCTTCTTGCCA  
 GCCCTGCCGGGCCACTTGTCTTCATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG  
 TGCAGAGGCAGTCTGGGCTTGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG  
 GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT  
 CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT  
 GCGCTGGAGAGAGCCACCGTCTTCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT  
 GGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGAGAAGTGGGCCAGGAGCCCCCTGC  
 TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
 CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCTCCAGCCCCG  
 GTTTTGGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACGTTCCGGC  
 CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACGGGACG  
 GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC  
 AGGCTACTGCCTGTCCACCAACTGCTCTTCTTCTCTGGGCCAGAATGAGGGGATGCACACAGG  
 GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC  
 AGAGCTGAGGCCATCGGATACGCCTACCCTACCCGGGACATCTTCATGGAAAACATCATGTTCTG  
 TGGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
 AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
 TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT  
 TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGC  
 AATTCTCTTGCTCATCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACCTGGCTAAT  
 TTTTATATTTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT  
 CTCAAGAGATCCGCCCACCTCAGGCTCCCAAAGTGTGGGATTATTAGGTGTGAGCCACCGTGTCTG  
 GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC  
 ATGGGGGCTCTCTCCCCTAGATGGCTGCTCCTCCCAACACAGCCACAGCAGTGGCAGCCCTGG  
 GTGGCTTCTATACATCTTGGCAGAATACCCCCAGCAAACAGAGAGCCACACCCATCCACACCG  
 CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC  
 TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG  
 ATAAGCAAAGCCACCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
 GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

**FIGURE 134**

MSARGRWEGGRRACRGSGLLARAQGAERTVSSEQRPAMASLGLLLLLLTALPPLWSSSLPGLD  
 TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV  
 GMLGEKLEAAIQRSYLKLSDPKYLRREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPDQSFSEE  
 RSDVCLVQLLGTGTDSSSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQSQD  
 YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMMGGFSDFYKLRWLEAILSWQKQEGCGF  
 EPDAEDEELSKAIQYQQHFSSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSLILP  
 SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPTSGSQSVGL

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

**FIGURE 135**

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG  
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGGGAGG  
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGC  
CTCAGGACTGGATCTCGGCGGCCCGAGTGTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAG  
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCTCC  
AGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG  
TGAATTACATCAAAACATCAGAGGTGTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT  
CCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT  
TATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC  
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT  
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG  
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTTCAC  
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAACCGTGTGAAGCAACTACTATAAACTT  
GAGTCATCCCGACGTTGATCTCTTACAACGTGTGTATGTT  
AACTTTTGTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTGTCTGTAT  
GAGGTCAATATTGATGTCACCTGAATTAATTACAGTGCTCTATAGAAAATGCCATTAATAAATTAT  
ATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAEGSGGSGVGIGDRFKIEGRAVVPGVKPDWISAA  
 RVLVDGEEHVGFLKTDGSFVVDIPSGSYVVEVVSFAYRFDPPVRVDITSGGKMRARYVNYIKTSE  
 VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLI FVLLPKVVNTSDPDMRREME  
 QSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSKTGKSGAGKRR

**Important features of the protein:**

**Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

**FIGURE 137**

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA  
 CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAAACAA  
 GTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC  
 CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC  
 CACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTTTCACGGGAGGCTTGGCAGT  
 TTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCCTCTAGTCTGCTTCAGC  
 CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG  
 AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG  
 TGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTGCAAGACACA  
 AAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAA  
 AACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA  
 CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG  
 AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC  
 TTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTG  
 CTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA  
 ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG  
 CTTCCCTGCGATGATTGTCTTTATGCATCCCCAATCTTAATGAGACCATACTTGTATAAGATTTT  
 TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTATTTA  
 ATGTATTTATTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTG  
 ACTAGAGCAGGTGATGTATTTTATACAGTAAAAAAAACCTTGTAATTTCTAGAAGAGTGG  
 CTAGGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT  
 ATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTGTGATGTGAATGACAC  
 ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAG  
 CCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTCTTTGCATACCAAAAAAA  
 AAAAAAAAAA

**FIGURE 138**

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGATTTCATNSHSDSELRPEIF  
SSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS  
SLANSFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAQAVVKALGELDILLQWMEET  
E

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 139**

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCAGCC  
 TAGCGTGTCACGATGCGGCTGGGCTCCGGGACTTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC  
 TAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTTCGTTCTCTGCCAGAGCGGAA  
 CACGGAGCGGAGCCCCAGCGCCCGAACCTTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC  
 ACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTG  
 GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGAAAAAGGAGCATCTCACAGT  
 TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG  
 CCTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATTCCTGCACTGCTGGAAGACAGTGTGA  
 TAAGACAAGCAAAAGCAGCTGGA AAAAGAATAGTCTTTATGGAGATGAAACCTGGGTAAATTA  
 TTCCCAAAGCATTTTGTGGAATATGATGGAACAACCTCATTTTTCGTGTCAGATTACACAGAGGT  
 GGATAATAATGTACAGAGGCATTTGGATAAAGTATTA AAAAGAGGAGATTGGGACATATTAATCC  
 TCCACTACCTGGGGCTGGACCACATTGGCCACATTTCAGGGCCCAACAGCCCCCTGATTGGGCAG  
 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGA  
 AGCGCCTTTACCCAATTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG  
 GGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAA  
 CCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGC  
 ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGAC  
 CAATGAGAGAGCAGTTGAGATTTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAG  
 AATGTGCCGTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGG  
 GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCCTATTCAACCTGGGCTCCAAGG  
 TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCCAG  
 TTCTCACCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAAGGCTGAGCTGGAAGTCCCA  
 CTGTCTCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGCCGTTACAGT  
 CATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGCAGGCT  
 GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGGCAGTGCCCTGGAC  
 AGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCCGACACAGGTG  
 TTCACATCTGTGCTGTGAGGTGAGATGCCTCAGTTCTTGGAAGCTAGGTTCCCTGCGACTGTTAC  
 CAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA  
 TCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA  
 CACTCAGGAGGGTCAAAAGGAGACTTGGTCGCACCACTCATCCTGCCACCCCCAGAATGCATCCT  
 GCCTCATCAGGTCCAGATTTCTTTCCAAGCGGACGTTTCTGTTGGAATTCTTAGTCCTTGCC  
 TCGGACACCTTCATTGCTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC  
 ACTCAGATCCACAGAGCCAGGATCAAGGGACCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC  
 ACCCCAACCTGCACAGCCCTCATCCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGT  
 CTGACCGAGACACTCACAGCTTTGTATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTG  
 CCACGCTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAG  
 CTGCACACAGTATGTAGTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

**FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPPLF  
SKVVIVLIDALRDDFVFGSKGVKFPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWWKLFPKHFVEYDGTTSTFFVSDYTEVDNNV  
TRHLDKVLKRGDWDILILHYLGLDHHIGHISGPN SPLIGQKLEMDSVLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 58-76

**N-glycosylation sites.**

amino acids 56-60, 194-198

**N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

**Amidation site.**

amino acids 154-158

**Cell attachment sequence.**

amino acids 205-208



**FIGURE 141**

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA  
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAAC  
TCCCTATAGAAAACAACTGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC  
CCGAAGAAATTCAGCATTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT  
AGCAGTTCCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT  
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGTCTCTAAAGGGAGTTTTGTCTCTAC  
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT  
GGCTGCCCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA  
ACATGCTGGAGTCGGCGGCTCACCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT  
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAA  
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA  
ATTTGAACTAATTGTATAAAAACACCAAACCTGCTCACT

**FIGURE 142**

MLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEI  
FFALASSLSSASAEKGSPIILGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFI  
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.  
amino acids 33-36

N-myristoylation site.  
amino acids 50-55, 87-92

Interleukin-1  
amino acids 37-182

**FIGURE 143**

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA  
TCCAGGATCCTGTCCTTCCTGTCCTGTAGGAGTGCCTGTTGCCAGTGTGGGGTGAGACAAGTTTG  
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTCTGTGGG  
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG  
AAGGGAGGTCTGTCCTGGGCGCTGCTGCTGCTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC  
CTGGCATTTCACAGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG  
CACATCTTGAATTCCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACGCCATTTCCAAGAAAGCACAG  
AGCTGAACAATACTTTCACCTGCTTCTTCACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC  
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTTGAGTGAAACCCACTCACAGGCTTGTCCATGT  
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT  
TTGGACTTGTTTGTTATCCTATTTTGCATGTGTTTGAGATCTCAGATCAGTGTTTTAGAAAATCC  
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGCATTTTAAGAAAAAAAAAA  
AAA

**FIGURE 144**

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTGKGFEDDIDNCHFQUESTLNNTFTCFFTISTRP  
WMTQFSLLNKTCLGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristoylation site.**

amino acids 9-15

**FIGURE 145**

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG  
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCAGCACTGCCCAGATCA  
CTGAGGCCAGGTGGCTGAGAACCGCCCGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT  
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA  
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCTGCATCAATGCCA  
CCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT  
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT  
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT  
CTTCTCCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGCGGCGATGCACTCGCACTGCAAA  
TGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT  
CCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT  
GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG  
GTGTATTCCCGTTTTACAGATAAGGAACTGAGGCCAGAGAGCTGAAGTACTGCACCCAGCATC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCTGGCTTGCTAACCCAGGTTTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT  
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSWWLATVCMLLFSLHSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK  
 LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ  
 VLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMLVK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

**FIGURE 147**

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATTT  
CCTGATGATTTATAGACTCAAAGAAAACTATGTTTCAGAAGCTCTCTTCTTTCTGGCCTCCTCT  
CTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
AAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTTATTTTTTGAAATTT  
CAACTTTCAGATTCAGGGGGTACATGTGAAGGTTGTTTTATGAGTATATTGCATTGATGTGCTGAGG  
TTTGGGGT

### **FIGURE 148**

MFRSSLLFWPPLCLLSLFLILISSIYSECKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68



**FIGURE 149**

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGACTTGAC  
 TCCCGCGCGCCCCAACCTTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCGCCCGAGTCC  
 CGGCCCTCTCCCGCCCCACCCACCTCCTGGCTCTTCTGTTTTTACTCCTCCTTTTCATTCATA  
 ACAAAGCTACAGCTCCAGGAGCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGAAGAATGGGGTT  
 CCTCGGGACCGGCACTTGGATTCTGGTGTAGTGCTCCCGATTCAAGCTTTCCCCAACCTGGAGGAA  
 GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA  
 GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTT  
 TGTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA  
 TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTG  
 ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA  
 TCACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG  
 AAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC  
 CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAAATTAATCTCAAAGGAAGCCAACAA  
 TTATGAGGAGGATCCCAATAAGCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG  
 TGACTCCAATGGCAGCAATTCAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA  
 TTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGACAACCTTGAGGAACTCCA  
 ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAAGCAAAAGAGAAAGAAA  
 CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT  
 CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT  
 AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA  
 CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA  
 GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC  
 CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTT  
 CAAAGATGAGAGACTTCATCAATAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA  
 GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAAAAGATCCAGGAGTCTTTCAA  
 CTGTTTCAGAAAACATAATATAGCTTAAAACACTTCTAATTCTGTGATTAAAATTTTTTGACCCAAGG  
 GTTATTAGAAAGTGTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAAACATAGCTTTCTTCCC  
 GTAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

**FIGURE 150**

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG  
 QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDYDSTKSGLDHK  
 FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE  
 VLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNTLTLTNGLE  
 RRTKTYSEDNFEELQYFFNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISP EEGV  
 SYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEEAAKMEKEYGSLKDKSTKDD  
 NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFINKQADAYVEKGILDK  
 EEAEAIKRIYSSL

**N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
 220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
 341, 369-372, 382-385, 386-389, 387-390

**N-myristoylation sites:**

amino acids 143-148, 239-244

**FIGURE 151**

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCTGTGGAGCTCAA  
 GATGGTCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC  
 ATAATAACCAAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC  
 GTGGTCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCTGGGTGTCCAGGGTGGGAG  
 CCAGTGCTGTATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG  
 AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACC  
 TCCAGCTTCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCC  
 TGTCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACTTCC  
 AGCAGTGTGACTAGGGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT  
 GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTGCTCTCAGGACCCCACTGCTGACTTAG  
 TGGGCACCTGACCACTTTGTCTTCTGGTTCCCAAGTTTGGATAAATTCTGAGATTTGGAGCTCAGT  
 CCACGGTCTCCCCACTGGATGGTGCTACTGCTGTGGAACCTTGTAACCATGTGGGGTAAA  
 CTGGGAATAACATGAAAAGATTTCTGTGGGGTGGGGTGGGGGAGTGGTGGGAATCATCTCTGT  
 TAATGGTAACTGACAAGTGTACCTTGAGCCCCGAGGCCAACCATCCCCAGTTGAGCCTTATA  
 GGGTCAGTAGCTCTCCACATGAAGTCTGTCACTCACCAGTGTGCAGGAGAGGGAGGTGGTCATA  
 GAGTCAGGGATCTATGGCCCTTGGCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCTATA  
 TGCTACCTTTCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTATGTCAGAA  
 GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCTCTTTTAAAAACCCAA  
 GATACAATCAAAATCCAGATGCTGGTCTCTATTCCCATGAAAAGTGCTCATGACATATTGAGA  
 AGACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTTAAAGATACTTATTTATATATT  
 TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTGAGGGTGGTGGCAGTAT  
 AGGTGATTTTCTTTTAAATTTCTGTAAATTTATCTGTATTTCTTAATTTTCTACAATGAAGATGA  
 ATTCTTTGTATAAAAAAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA  
 TTGTCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG  
 TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT  
 GTGGCTGGAATCTCTGGGTAAGGAACTTAAAGAACAATAATCATCTGGTAATTTCTTCTAGAAAG  
 GATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA  
 ATTGTGTCCCCCTCAAATTCACATCTTCTTGGAACTCAGTCTGTGAGTTTATTTGGAGATAAG  
 GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCTGCTGGATGAAGGTAGACCTAAATTCATATAT  
 GACTGGTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA  
 AAGATGAAGGCAGAGATCGGAGTTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC  
 ATCAGAAGCTTGGAAGAGGCAAAGAAGAAATTTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG  
 CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGATAAATTTCCGGCTGTTTTAA  
 GCCACCAAGGATAAATGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAATGATCCCTGT  
 CTCCTCGTGTTTACATTCTGTGTGTGTCCCCCTCCACAATGTACCAAAGTTGTCTTTGTGACCAA  
 TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC  
 TACTTGAGCCCTCTCTCTGCCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG  
 AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT  
 GCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT  
 AAGTTGCTCAGTTTTGGTCTAACTTGTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

**FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWLDASLSPVILGVQGGG  
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGAWNAPITDFYFQQCD

**N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

**Interleukin-1 signature.**

amino acids 111-131

**Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103

**FIGURE 153**

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC  
CCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTCTTG  
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC  
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA  
CAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACTTCACCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTT  
CAGCCTTATATGCAGGAGGTGGTGGCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTTATGTCTCTGAGAAAT  
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCTTGCTAGAAATAA  
CAATTAGATGCCCCAAAGCGATTTTTTTTAAACCAAAAGGAAGATGGGAAGCCAACTCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA  
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTATTGTAAGTGGTGTTC  
TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT  
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA  
TGTATTTATTATTATTATAAGACTGCATTTTATTATATCATTTTATTAATATGGATTTATTAT  
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT  
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

**FIGURE 154**

MAALQKSVSSFLMGTLATSCLLLLLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL  
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLPQSDRFQPYMQEVVPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

**FIGURE 155**

GGCTTGCTGAAAATAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT  
CAGTCAGTGCCCCGACTTGTGACTGAGTGTGCAGTGCCCAGCATGTACCAGGTCAGTGCAGAGGGC  
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC  
TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT  
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCAT  
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGG  
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCTAGAGCCTGCTAG  
GCCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCAGGACCTGTACCACGCCGT  
TGCCCTGTGCCCCGCACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGGGCAACTCGGA  
GCTGCTCTACCACAACCAGACTGTCTTCTACAGCGGCCATGCCATGGCGAGAAGGGCACCCACA  
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGTGCGGCCCCGT  
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTTGGGAAACCTGGAGCCAGGTGTACA  
ACCACTTGCCATGAAGGGCCAGGATGCCCAGATGCTTGGCCCCCTGTGAAGTGTGTCTGGAGCAG  
CAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAAAACCTGCACTTCTGCACATTTTGAAAAGAG  
CAGCTGCTGCTTAGGGCCGCCGAAGCTGGTGTCTGTCTCTCTCAGGAAAGGTTTTCAAA  
GTTCTGCCCATTTCTGGAGGCCACCACTCCTGTCTCTTCCTCTTTCCCATCCCCTGCTACCCTG  
GCCCAGCACAGGCACTTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATT  
TGTTTTGTTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT  
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTTATCCAAATAAATAT  
CTTTATTTAAAAATGAAAAA

**FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPSKGQDTSEELLRWSTVPVPPLLEPA  
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTKGYCLERRLYRVSLACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156



**FIGURE 157**

CCGGCGATGTCGCTCGTGTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC  
 GACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC  
 CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTC  
 ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAA  
 GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGG  
 CCTTCCAGACTCAGACCAGACCTCTGGTGGTAAATGGACATTTTCCTACATCGGCTTCCCTGTA  
 GAGCTGAACACAGTCTATTTTCATTGGGGCCATAATATTCCTAATGCAAATATGAATGAAGATGG  
 CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA  
 AGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTTGTGAAGAAGATGAGGAGACA  
 GTAGAAGTGAACCTCACAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC  
 TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA  
 TTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC  
 AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCT  
 GGATAACAACAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCTGCTGTCTGTGCTGGTGCCA  
 CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT  
 TCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA  
 TCACACAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCATCCTTGAAA  
 AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCA  
 GCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA  
 GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCA  
 GTGATCTAAGAAGCCAGATTTCATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA  
 AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT  
 CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACG  
 ATGGCTGTGCTCCTTGTAG

**FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLRDLRVEPVTTSVATGDYSILMNVSWV  
 LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
 NANMNEDGPSMSVNFSPGCLDHIMYKKKCVKAGSLWDPNITACKNEETVEVNFTTTPLGNRYMALIQH  
 STIIGFSQVFEPHQKKQTRASVVIPTVDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVFPPLDNNK  
 SKPGGWLPLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL  
 QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGPSSENSQDLFPLA  
 FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD  
 GCCSL

**Important features of the protein:****Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283  
 - 287

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-452

**FIGURE 159**

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCTTTCTGAGTGAGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA  
CTTTTTTCCAAAAGCCTGAGAGTTGCCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
GAATTACACTGTCACCTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA  
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT  
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

**FIGURE 160**

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN  
QRVSMERNIESRSTSPWNYTWTWDPNRYPSSEVVQAQCRNLGCINAQKEDISMNSVPIQQETLVV  
RRKHQGCSSVSFQLEKVLVTVGCTCVTPVIHHVQ

**Signal sequence:**

amino acids 1-30

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 106-111, 136-141

**FIGURE 161**

A C A C T G G C C A A C A A A A A C G A A A G C A C T C C G T G C T G G A A G T A G G A G G A G A G T C A G G A C T C C C A G G  
 A C A G A G A G T G C A C A A A C T A C C C A G C A C A G C C C C C T C C G C C C C C T C T G G A G G C T G A A G A G G G A T T C  
 C A G C C C C T G C C A C C C A C A G A C A C G G G C T G A C T G G G G T G T C T G C C C C C C T T G G G G G G G G C A G C A C  
 A G G G C C T C A G G C C T G G G T G C C A C C T G G C A C C T A G A A G A T G C C T G T G C C C T G G T T C T T G C T G T C C T  
 T G G C A C T G G G C C G A A G C C C A G T G G T C C T T T C T C T G G A G A G G C T T G T G G G G C C T C A G G A C G C T A C C  
 C A C T G C T C T C C G G G C C T C T C C T G C C G C C T C T G G G A C A G T G A C A T A C T C T G C C T G C C T G G G G A C A T  
 C G T G C C T G C T C C G G G C C C C G T G C T G G G C C C T A C G C A C C T G C A G A C A G A G C T G G T G C T G A G G T G C C  
 A G A A G G A G A C C G A C T G T G A C C T C T G T C T G C G T G T G G C T G T C C A C T T G G C C G T G C A T G G G C A C T G G  
 G A A G A G C C T G A A G A T G A G G A A A G T T T G G A G G A G C A G C T G A C T C A G G G G T G G A G G A G C C T A G G A A  
 T G C C T C T C T C C A G G C C C A A G T C G T G C T C C T T C C A G G C C T A C C C T A C T G C C C G T G C G T C C T G C  
 T G G A G G T G C A A G T G C C T G C T G C C C T T G T G C A G T T T G G T C A G T C T G T G G G C T C T G T G G T A T A T G A C  
 T G C T T C G A G G C T G C C C T A G G G A G T G A G G T A C G A A T C T G G T C C T A T A C T C A G C C C A G G T A C G A G A A  
 G G A A C T C A A C C A C A C A C A G C A G C T G C C T G C C C T G G C T C A A C G T G T C A G C A G A T G G T G A C A  
 A C G T G C A T C T G G T T C T G A A T G T C T C T G A G G A G C A G C A C T T C G G C C T C T C C C T G T A C T G G A A T C A G  
 G T C C A G G G C C C C C A A A A C C C C G G T G G C A C A A A A C C T G A C T G G A C C G C A G A T C A T T A C C T T G A A  
 C C A C A C A G A C C T G G T T C C C T G C C T C T G T A T T C A G G T G T G G C C T C T G G A A C C T G A C T C C G T T A G G A  
 C G A A C A T C T G C C C C T T C A G G G A G G A C C C C G C G C A C A C C A G A A C C T C T G G C A A G C C G C C C G A C T G  
 C G A C T G C T G A C C C T G C A G A G C T G G C T G C T G G A C G C A C C G T G C T C G C T G C C C G C A G A A G C G G C A C T  
 G T G C T G G C G G G C T C C G G G T G G G G A C C C C T G C C A G C C A C T G G T C C C A C C G C T T T C C T G G G A G A A C G  
 T C A C T G T G G A C A A G G T T C T C G A G T T C C C A T T G C T G A A A G G C C A C C C T A A C C T C T G T G T T C A G G T G  
 A A C A G C T C G G A G A A G C T G C A G C T G C A G G A G T G C T T G T G G G C T G A C T C C C T G G G G C C T C T C A A A G A  
 C G A T G T G C T A C T G T T G G A G A C A C A G A G C C C C A G G A C A A C A G A T C C C C T C T G T G C C T T G G A A C C C A  
 G T G G C T G T A C T T C A C T A C C C A G C A A A G C C T C C A C A G A G G C A G C T C G C C T T G G A G A G T A C T T A C T A  
 C A A G A C C T G C A G T C A G G C C A G T G T C T G C A G C T A T G G G A C G A T G A C T T G G G A G C G C T A T G G G C C T G  
 C C C C A T G G A C A A T A C A T C C A C A A G C G C T G G G C C C T C G T G T G G C T G G C C T G C C T A C T C T T T G C C G  
 C T G C G C T T T C C C C T A T C C T C C T T C T C A A A A A G G A T C A C G C G A A A G G G T G G C T G A G G C T C T T G A A A  
 C A G G A C G T C C G C T C G G G G C G G C C G C A G G G G C C G C G G C T C T G C T C C T A C T C A G C C G A T G A  
 C T C G G G T T T C G A G C G C C T G G T G G G C G C C C T G G C G T C G G C C C T G T G C C A G C T G C C G C T G C G C G T G G  
 C C G T A G A C C T G T G G A G C C G T C G T G A A C T G A G C G C G C A G G G G C C C G T G G C T T G G T T T C A C G C G C A G  
 C G G C G C C A G A C C C T G C A G G A G G G C G G C G T G G T G G T C T T G C T C T T C T C C C G G T G C G G T G G C G C T  
 G T G C A G C G A G T G G C T A C A G G A T G G G G T G T C C G G G C C G G G G C G C A C G G C C G C A C G A C G C C T T C C  
 G C G C C T C G C T C A G C T G C G T G C T G C C C G A C T T C T T G C A G G G C C G G G C G C C C G G C A G C T A C G T G G G G  
 G C C T G C T T C G A C A G G C T G C T C C A C C C G A C G C C G T A C C C G C C C T T T C C G C A C C G T G C C C G T C T T  
 C A C A C T G C C C T C C C A A C T G C C A G A C T T C C T G G G G G C C C T G C A G C A G C C T C G C G C C C C G G T T C C G  
 G G C G G C T C C A A G A G A G A G C G G A G C A A G T G T C C C G G G C C C T T C A G C C A G C C C T G G A T A G C T A C T T C  
 C A T C C C C C G G G G A C T C C C G C G C C G G A C G C G G G T G G G A C C A G G G G C G G G A C C T G G G G C G G G G A  
 C G G G A C T T A A A T A A A G G C A G A C G C T G T T T T C T A A A A A A

**FIGURE 162**

MPVPWFLLSLALGRSPVVLSELERLVGPQDATHCSPGLSCRLWSDILCLPGDIVPAPGPFVLAPTHLQTELV  
 LRCQKETDCDLCRLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEV  
 QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTPRYEKELNHTQQLPALPWLNVSAADGNVHLVLNV  
 EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ  
 LWQAARLRLTLQSWLLDAPCSLPAAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFLLKGHPNLCVQ  
 VNSSEKLQEQECLWADSLGPKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS  
 GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSAAAARG  
 RAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSP  
 GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVET  
 LPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

**Signal sequence:**

amino acids 1-20

**Transmembrane domain.**

amino acids 453-475

**N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,  
 334-337, 357-360, 391-394

**Glycosaminoglycan attachment site.**

amino acids 583-586

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

**N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,  
 692-697, 696-701, 700-705

**FIGURE 163**

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGC'TGCT'GACCATCTTGACTGTGGGATCCCTGGCT  
 GCTCACGCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCAGTCCAGCAACTTTGA  
 AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA  
 AGACGTACGGAGAGAGGGGACTGGGTGGCAAAGAAGGGCTGTGTCAGCGGATCACCCGGAAGTCCTGC  
 AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT  
 GTCAGTGCGGGAGGCCGGTCAGCCACCAAGATGACTGACAGGTTGAGTCTCTGTCAGCACACTAC  
 CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCATCCTA  
 CCCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCC'TGGAAGACATCTTCCATGACCTG  
 TTCTACCACCTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA  
 ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCCTTGGCACCATCATGATTGCGTTCCCA  
 CCTGGGCCAAGGAGAGTGCCCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC  
 TACTCCTTCTCCGGAGCCTTCTGTCTCCATGGGCTTCTCTGTCGACGTACTCTGCTACCTGAG  
 CTACAGATATGTACCAAGCCGCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCTTGACTT  
 TCCAGCCGCTGCGCTTCATCCAGGAGCACGTCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC  
 AGTCTGGCCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC  
 TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC  
 CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCAAACGCTGCCCTGAG  
 GTCGGGCCCCCATCCTATGCACCTCAGGTGACCCCGAAGCTCAAT'TCCCATTCTACGCCCCACA  
 GGCCATCTCTAAGGTCCAGCCTTCTCCTATGCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT  
 CCTATGGGGTATGATGGAAGGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCTCTAAA  
 CACCTTAGGCCTAAAGGTGAGCTTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT  
 TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCAGC  
 CCCTGGGGATTTGCACAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGGACA  
 CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC  
 CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC  
 TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCCCTGAGACCTCAGACCTG  
 GAGCAGCCACAGAACTGGATTCTCTTTTCAGAGGCTGGCCCTGACTGTGTCAGTGGGAGTCCCTG  
 AGGGGAATGGGAAAGGCTTGGTGCTTCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA  
 ATCCCATGCTGCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC  
 AGAGGGAGTGGCATGCAGGGCCCCCTGCCATGGGTGCGCTCCTCACCAGGAACAAGCAGCATGATA  
 AGGACTGCAGCGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGCTCGCTGAGCCCTG  
 CAAGGCAGAAATGACAGTGCAAGGAGGAAATGCAGGGAAACTCCCGAGGTCCAGAGCCCCACCTC  
 CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCCTCTCCTTGCCCCATTCTTGCCAGTTTC  
 ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCTTCTGTGTCATTGTTCAAAGGTGGGAAGAGA  
 GCCTGGAAAAGAACCAGGCCCTGGAAGAAGCAAGAGGAGGCTGGGCAGAACCAGAACAACTGC  
 ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA  
 TTCCCAGCCAGGGCAACTGCCTGACGTTGCACGATTCAGCTTCATTCTCTGATAGAACAAGC  
 GAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTTCTGCAGGCAGGAGTTTCAGACCT  
 ATCCTGAGAATGGGGTTTGAAAGGAAGGTGAGGGCTGTGGCCCCCTGGACGGGTACAATAACACAC  
 TGTACTGATGTCAAACTTTGCAAGCTCTGCCTTGGGTTTCAAGCCATCTGGGCTCAAATTCAGC  
 CTCACCACTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTTCCTC  
 ATCTGTAATGTGGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG  
 TCTTTAAAGTGCTTAATAGTGCCTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA  
 AAAAAAA

**FIGURE 164**

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW  
VAKKGCQRITRKSCNLTIVETGNLTelyyARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTCTIS  
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRITYQMHLGGKQREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLESMGFLVAVLCYLSYRYVTKPPAP  
PNSLNVQRVLTfQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISIQLPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSSY  
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGLSLQEVTSIAM  
EESQEAksLHQPLGICTDRtSDPNVLHSGEETpQYLKGQLPLLSSVQIEGHPMSLPLQPPSGPC  
SPSDQGPSPWGLLESIVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTQWES

**Signal sequence.**

amino acids 1-17

**Transmembrane domain.**

amino acids 233-250

**N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

**N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570



**FIGURE 165**

TGGCCTACTGGAAAAAAAAAAAAAAAAAAGTCACCCGGGCGCCGGTGGCCACAACATGG  
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG  
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT  
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCCTGATTGTCGTTTTGTGAATTTTA  
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACCTTGGGCTGGA  
AGTGTGAAACACAGTTTTGGATATTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA  
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT  
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAACGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA  
ACTTGACCCTGTGCCTGAGCCCGAGGCATTGAGAGCTGATTGAGAGGATGGAGAAGGTGCTTTCT  
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT  
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCTGCACGATAA  
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA  
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT  
CATTACAGCAAAGGATTCGTTGGCATCAAATCTAAGTTTGTGTTTACAAAGATTGTTTTTAGTA  
CTAAGCTGCCTTGGCAGTTTGCAATTTTGAGCCAAACAAAAATATATTATTTCCCTTCTAAGTA  
AAAAAAAAAAAAAAAAAAAA



**FIGURE 167**

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTGTCAGAGGCCGGGGAAGAGAAGCAAAGCGC  
 AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCTCTAGGACATACACGGGACCCCTAACTTC  
 AGTCCCCCAAACGCGCACCTCGAAGTCTTGAACCTCCAGCCCCGCACATCCACGCGCGGCACAGG  
 CGCGGCGAGGCGGCGAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTCCGGGAGCTGGGCTCGGGC  
 GGGGGGAGTAGGGCCCGGCAGGGAGGCGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG  
 GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCGCGGATGAGCCGCTGG  
 TCTCGTGTCTGCTGGGCGCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCGCGCGCTGGTCAGC  
 GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAACT  
 GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCTGGCTTGTGAGAGTGAGGGAGGAGTCCCTCTCA  
 GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG  
 ACAGGGATTTCTGATGGTGATTCTCGGATAGGGCTTTGGAGGAATGGAGATGGGCAAACATCTGG  
 TGCCGTGCCAGATCTCTACCAAGTGGTCTGATGGAAGCAATTCCAGTACCGAACTGGTACACAG  
 ATGAACCTTCCTGCGGAAGTGAAAAGTGTGTTGTGATGTATCACCACCAACTGCCAATCCTGGC  
 CTTGGGGGTCCCTACCTTTACCAAGTGAATGATGACAGGTGTAACATGAAGCACAATTATATTTG  
 CAAGTATGAACCAGAGATTAATCCACAGCCCCGTAGAAAAGCCTTATCTTACAAATCAACCAG  
 GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGT  
 ATACCAACAATAACCCCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCT  
 GCATAAAAGTAAAGGAAGAACAACAACTAGTCCAAACAGTCTACACTGTGGATTCAAAGAGTA  
 CCAGAAAAGAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCCAGAAATTTGTAATCT  
 GGATCTGTATAAGGAATGGCATCAGAACAATAGCTTGAATGGCTTGAATCACAAGGATCTGC  
 AAGATGAACTGTAAGCTCCCCCTTGAGGCAAAATATAAAGTAATTTTATATGTCTATTATTTCA  
 TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAA  
 ACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTATCAACACGTCGGGAGTA  
 TGTGTGTTAGAAGCAATTCCTTTTATTTCTTTACCTTTCATAAGTTGTTATCTAGTCAATGTAA  
 TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTGCATAAGTGTTTGATAAAA  
 ATGAAGTGTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAAG  
 AAAGTATTACTGTTGTCAACTGAATTCACACACACAAATATAGTACCATAGAAAAAGTTTGT  
 TTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGA  
 AATAAGAAGCTATTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGCAAGGAT  
 TGTCTAATTTCAATTTGCAAGACATGTGCCTTATAATTTATTTTAGCTTAAATTAACAGATT  
 TTGTAATAATGTAACCTTGTAAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG  
 TGACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA  
 GGGTCTGAAATCAATGTGGTCCCTCTCTTGGCCACTAAACAAAGATGGTTGTTCCGGGGTTTGGG  
 ATTGACACTGGAGGCAGATAGTTGCAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG  
 ACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG  
 ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAATGGGTTGG  
 AACCATCAGTGATCGCATATTCATTGATGAGGGTTGCTTGAGATAGAAAATGGTGGCTCCTTT  
 CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCCTTGTCTTCTCAAGAGAAAGTTGTAACCT  
 CTGGTCTTCATATGTCCCTGTGCTCCTTTTAAACCAATAAAGAGTTCTTGTCTTCTGGGGGAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 168**

MSRVVSLLLGAALLCGHGAFCRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESE  
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ  
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK  
PYLTNQPGDTHQNVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSkgRtKtSPNQ  
STLWISKSTRKESGMEV

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-  
145, 212-217